



Europäisches Patentamt
European Patent Office
Office européen des brevets



(11)

EP 1 310 571 B1

(12)

EUROPEAN PATENT SPECIFICATION

(45) Date of publication and mention
of the grant of the patent:
15.02.2006 Bulletin 2006/07

(51) Int Cl.:
C12Q 1/70^(2006.01) **C07K 14/015^(2006.01)**
C12N 15/86^(2006.01) **C12N 15/10^(2006.01)**
C12Q 1/68^(2006.01) **C12N 5/10^(2006.01)**

(21) Application number: **02257826.4**

(22) Date of filing: **12.11.2002**

(54) **A Method of identifying unknown adeno-associated virus (AVV) sequences and a kit for the method**

Verfahren zur Identifizierung von Adeno-assoziiertem Virus (AAV) Sequenzen sowie Kit zur Ausführung der Methode

Une méthode d'identification de séquences de virus adéno-associés et kit permettant d'appliquer la méthode

(84) Designated Contracting States:
**AT BE BG CH CY CZ DE DK EE ES FI FR GB GR
IE IT LI LU MC NL PT SE SK TR**
Designated Extension States:
AL LT LV MK RO SI

(30) Priority: **13.11.2001 US 350607 P**
17.12.2001 US 341117 P
01.05.2002 US 377066 P
05.06.2002 US 386675 P

(43) Date of publication of application:
14.05.2003 Bulletin 2003/20

(73) Proprietor: **THE TRUSTEES OF THE UNIVERSITY
OF PENNSYLVANIA**
Philadelphia,
Pennsylvania 19104-6283 (US)

(72) Inventors:
• **Gao, Guangping**
Rosemont, Pennsylvania 19010 (US)
• **Wilson, James M.**
Gladwyne, Pennsylvania 19035 (US)
• **Alvira, Maricio**
Philadelphia, Pennsylvania 19104 (US)

(74) Representative: **Hale, Stephen Geoffrey et al**
Bromhead Johnson,
Kingsbourne House,
229-231 High Holborn
London WC1V 7DP (GB)

(56) References cited:
WO-A-02/18659

- **GAO GUANG-PING ET AL: "Novel adeno-associated viruses from rhesus monkeys as vectors for human gene therapy." PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES, vol. 99, no. 18, 3 September 2002 (2002-09-03), pages 11854-11859, XP002229849 <http://www.pnas.org> September 3, 2002 ISSN: 0027-8424**
- **FORSLUND OLA ET AL: "A broad range of human papillomavirus types detected with a general PCR method suitable for analysis of cutaneous tumours and normal skin." JOURNAL OF GENERAL VIROLOGY, vol. 80, no. 9, 1999, pages 2437-2443, XP002229850 ISSN: 0022-1317**
- **XIAO WEIDONG ET AL: "Gene therapy vectors based on adeno-associated virus type 1." JOURNAL OF VIROLOGY, vol. 73, no. 5, May 1999 (1999-05), pages 3994-4003, XP002229851 ISSN: 0022-538X**
- **GENE THERAPY, vol. 10, 2003, pages 194-196,**
- **PROC. NATL. ACAD. SCI. USA, vol. 100, no. 10, 2003, pages 6081-6086,**
- **J. VIROL., vol. 78, no. 12, 2004, pages 6381-6388,**

Note: Within nine months from the publication of the mention of the grant of the European patent, any person may give notice to the European Patent Office of opposition to the European patent granted. Notice of opposition shall be filed in a written reasoned statement. It shall not be deemed to have been filed until the opposition fee has been paid. (Art. 99(1) European Patent Convention).

EP 1 310 571 B1

Description

BACKGROUND OF THE INVENTION

[0001] Adeno-associated virus (AAV), a member of the Parvovirus family, is a small nonenveloped, icosahedral virus with single-stranded linear DNA genomes of 4.7 kilobases (kb) to 6 kb. AAV is assigned to the genus, Dependovirus, because the virus was discovered as a contaminant in purified adenovirus stocks. AAV's life cycle includes a latent phase at which AAV genomes, after infection, are site specifically integrated into host chromosomes and an infectious phase in which, following either adenovirus or herpes simplex virus infection, the integrated genomes are subsequently rescued, replicated, and packaged into infectious viruses. The properties of non-pathogenicity, broad host range of infectivity, including non-dividing cells, and potential site-specific chromosomal integration make AAV an attractive tool for gene transfer.

[0002] Recent studies suggest that AAV vectors may be the preferred vehicle for gene therapy. To date, there have been 6 different serotypes of AAVs isolated from human or non-human primates (NHP) and well characterized. Among them, human serotype 2 is the first AAV that was developed as a gene transfer vector; it has been widely used for efficient gene transfer experiments in different target tissues and animal models. Gene therapy vectors based on adeno-associated virus type 1 have also been disclosed (Xiao et al. J. Virology; May 1999; pages 3994-4008). Clinical trials of the experimental application of AAV2 based vectors to some human disease models are in progress, and include such diseases as cystic fibrosis and hemophilia B.

[0003] A general PCR method suitable for detecting human papillomavirus types in cutaneous tumours and normal skin is known (Forslund et al J. of General Virology: 1999 80: P2437-2443).

[0004] What are desirable are AAV-based constructs for gene delivery.

SUMMARY OF THE INVENTION

[0005] In one aspect, the invention provides a novel method of identifying unknown AAV sequences from cellular DNAs of various human and non-human primate (NHP) tissues using bioinformatics analysis, PCR based gene amplification and cloning technology, based on the nature of latency and integration of AAVs in the absence of helper virus co-infection, the method being defined in claim 1 hereinafter.

[0006] In another aspect the invention provides a kit for use in the method of the invention, the kit being as defined in claim 23 hereinafter.

DETAILED DESCRIPTION OF THE INVENTION

[0007] In the present invention, the inventors have found a method which takes advantage of the ability of adeno-associated virus (AAV) to penetrate the nucleus, and, in the absence of a helper virus co-infection, to integrate into cellular DNA and establish a latent infection. This method utilizes a polymerase chain reaction (PCR)-based strategy for detection, identification of sequences of AAVs from DNAs from tissues of human and non-human primate origin as well as from other sources.

[0008] Nucleic acid sequences can be identified according to the method of the invention. One such adeno-associated virus is of the serotype, termed herein serotype 7 (AAV7). Other novel adeno-associated virus serotypes identified by the method include AAV10, AAV11, and AAV12.

[0009] Among particularly desirable AAV fragments which can be identified are the cap proteins, including the vp1, vp2, vp3, the hypervariable regions, the rep proteins, including rep 78, rep 68, rep 52, and rep 40, and the sequences encoding these proteins. Each of these fragments may be readily utilized in a variety of vector systems and host cells. Such fragments may be used alone, in combination with other AAV sequences or fragments, or in combination with elements from other AAV or non-AAV viral sequences. In one particularly desirable embodiment, a vector contains the AAV cap and/or rep sequences.

[0010] As described herein, alignments are performed using any of a variety of publicly or commercially available Multiple Sequence Alignment Programs, such as "Clustal W", accessible through Web Servers on the internet. Alternatively, Vector NTI utilities are also used. There are also a number of algorithms known in the art which can be used to measure nucleotide sequence identity, including those contained in the programs described above. As another example, polynucleotide sequences can be compared using Fasta, a program in GCG Version 6.1. Fasta provides alignments and percent sequence identity of the regions of the best overlap between the query and search sequences. For instance, percent sequence identity between nucleic acid sequences can be determined using Fasta with its default parameters (a word size of 6 and the NOPAM factor for the scoring matrix) as provided in GCG Version 6.1. Similar programs are available for amino acid sequences, e.g., the "Clustal X" program. Generally, any of these programs are used at default settings, although one of skill in the art can alter these settings as needed. Alternatively, one of skill in the art can utilize

another algorithm or computer program which provides at least the level of identity or alignment as that provided by the referenced algorithms and programs.

[0011] The term "substantial homology" or "substantial similarity," when referring to a nucleic acid, or fragment thereof, indicates that, when optimally aligned with appropriate nucleotide insertions or deletions with another nucleic acid (or its complementary strand), there is nucleotide sequence identity in at least about 95 to 99% of the aligned sequences. Preferably, the homology is over full-length sequence, or an open reading frame thereof, or another suitable fragment which is at least 15 nucleotides in length. Examples of suitable fragments are described herein.

[0012] The term "substantial homology" or "substantial similarity," when referring to amino acids or fragments thereof, indicates that, when optimally aligned with appropriate amino acid insertions or deletions with another amino acid, there is amino acid sequence identity in at least about 95 to 99% of the aligned sequences. Preferably, the homology is over full-length sequence, or a protein thereof, e.g., a cap protein, a rep protein, or a fragment thereof which is at least 8 amino acids, or more desirably, at least 15 amino acids in length. Examples of suitable fragments are described herein.

[0013] By the term "highly conserved" is meant at least 80% identity, preferably at least 90% identity, and more preferably, over 97% identity. Identity is readily determined by one of skill in the art by resort to algorithms and computer programs known by those of skill in the art.

[0014] The term "percent sequence identity" or "identical" in the context of nucleic acid sequences refers to the residues in the two sequences which are the same when aligned for maximum correspondence. The length of sequence identity comparison may be over the full-length of the genome, the full-length of a gene coding sequence, or a fragment of at least about 500 to 5000 nucleotides, is desired. However, identity among smaller fragments, e.g. of at least about nine nucleotides, usually at least about 20 to 24 nucleotides, at least about 28 to 32 nucleotides, at least about 36 or more nucleotides, may also be desired. Similarly, "percent sequence identity" may be readily determined for amino acid sequences, over the full-length of a protein, or a fragment thereof. Suitably, a fragment is at least about 8 amino acids in length, and may be up to about 700 amino acids. Examples of suitable fragments are described herein.

[0015] The AAV sequences and fragments thereof are useful in production of rAAV, and are also useful as antisense delivery vectors, gene therapy vectors, or vaccine vectors.

[0016] As described herein, the vectors containing the AAV capsid proteins are particularly well suited for use in applications in which the neutralizing antibodies diminish the effectiveness of other AAV serotype based vectors, as well as other viral vectors. The rAAV vectors are particularly advantageous in rAAV readministration and repeat gene therapy.

[0017] As used throughout this specification and the claims, the terms "comprising" and "including" and their variants are inclusive of other components, elements, integers, steps and the like. Conversely, the term "consisting" and its variants is exclusive of other components, elements, integers, steps and the like.

I. Methods of the Invention

A. Detection of Sequences Via Molecular Cloning

[0018] In one aspect, the invention provides a method of identifying target (unknown) nucleic acid sequences in a sample. This method is particularly well suited for detection of viral sequences which are integrated into the chromosome of a cell, e.g., adeno-associated viruses (AAV) and retroviruses, among others.

[0019] As used herein, a sample is any source containing nucleic acids, e.g., tissue, tissue culture, cells, cell culture, and biological fluids including, without limitation, urine and blood. These nucleic acid sequences may be DNA or RNA from plasmids, natural DNA or RNA from any source, including bacteria, yeast, viruses, and higher organisms such as plants or animals. DNA or RNA is extracted from the sample by a variety of techniques known to those of skill in the art, such as those described by Sambrook, *Molecular Cloning: A Laboratory Manual* (New York: Cold Spring Harbor Laboratory). The origin of the sample and the method by which the nucleic acids are obtained for application of the method of the invention is not a limitation of the present invention. Optionally, the method of the invention can be performed directly on the source of DNA, or on nucleic acids obtained (e.g., extracted) from a source.

[0020] The method of the invention involves subjecting a sample containing DNA to amplification via polymerase chain reaction (PCR) using a first set of primers specific for a first region of double-stranded nucleic acid sequences, thereby obtaining amplified sequences.

[0021] As used herein, each of the "regions" is predetermined based upon the alignment of the nucleic acid sequences of at least two serotypes (e.g., AAV) or strains (e.g., lentiviruses), and wherein each of said regions is composed of sequences having a 5' end which is highly conserved, a middle which is variable, and a 3' end which is highly conserved, each of these being conserved or variable relative to the sequences of at least AAV1-AAV6. The 5' and 3' ends are highly conserved over at least 18 base pairs (bp). However, one or both of the sequences at the 5' or 3' end may be conserved over more than 18 bp, more than 25 bp, more than 30 bp, or more than 50 bp at the 5' end. With respect to the variable region, there is no requirement for conserved sequences, these sequences may be relatively conserved, or may have less than 90, 80, or 70% identity among the aligned serotypes or strains.

[0022] Each of the regions may span about 100 bp to about 10 kilobase pairs in length, provided that the first region is at least 250 bp in length. However, it is particularly desirable that one of the regions is a "signature region", i.e., a region which is sufficiently unique to positively identify the amplified sequence as being from the target source. For example, in one embodiment, the first region is about 250 bp in length, and is sufficiently unique among known AAV sequences, that it positively identifies the amplified region as being of AAV origin. Further, the variable sequences within this region are sufficiently unique that can be used to identify the serotype from which the amplified sequences originate. Once amplified (and thereby detected), the sequences can be identified by performing conventional restriction digestion and comparison to restriction digestion patterns for this region in any of AAV1, AAV2, AAV3, AAV4, AAV5, or AAV6, or that of AAV7, AAV10, AAV11, AAV12, or any of the other novel serotypes identified by the invention, which is predetermined and provided by the present invention.

[0023] Given the guidance provided herein, one of skill in the art can readily identify such regions among other integrated viruses to permit ready detection and identification of these sequences. Thereafter, an optimal set of generic primers located within the highly conserved ends can be designed and tested for efficient amplification of the selected region from samples. This aspect of the invention is readily adapted to a diagnostic kit for detecting the presence of the target sequence (e.g., AAV) and for identifying the AAV serotype, using standards which include the restriction patterns for the AAV serotypes described herein or isolated using the techniques described herein. For example, quick identification or molecular serotyping of PCR products can be accomplished by digesting the PCR products and comparing restriction patterns.

[0024] Thus, in one embodiment, the "signature region" for AAV spans about bp 2800 to about 3200 of AAV 1 [SEQ ID NO:6], and corresponding base pairs in AAV 2, AAV3, AAV4, AAV5, and AAV6. More desirably, the region is about 250 bp, located within bp 2886 to about 3143 bp of AAV 1 [SEQ ID NO:6], and corresponding base pairs in AAV 2 [SEQ ID NO:7], AAV3 [SEQ ID NO:8], and other AAV serotypes. To permit rapid detection of AAV in the sample, primers which specifically amplify this signature region are utilized. However, the present invention is not limited to the exact sequences identified herein for the AAV signature region, as one of skill in the art may readily alter this region to encompass a shorter fragment, or a larger fragment of this signature region.

[0025] The PCR primers are generated using techniques known to those of skill in the art. Each of the PCR primer sets is composed of a 5' primer and a 3' primer. See, e.g., Sambrook et al, cited herein. The term "primer" refers to an oligonucleotide which acts as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product which is complementary to a nucleic acid strand is induced. The primer is preferably single stranded. However, if a double stranded primer is utilized, it is treated to separate its strands before being used to prepare extension products. The primers may be about 15 to 25 or more nucleotides, and preferably at least 18 nucleotides. However, for certain applications shorter nucleotides, e.g., 7 to 15 nucleotides are utilized.

[0026] The primers are selected to be sufficiently complementary to the different strands of each specific sequence to be amplified to hybridize with their respective strands. Therefore, the primer sequence need not reflect the exact sequence of the region being amplified. For example, a non-complementary nucleotide fragment may be attached to the 5' end of the primer, with the remainder of the primer sequence being completely complementary to the strand. Alternatively, non-complementary bases or longer sequences can be interspersed into the primer, provided that the primer sequence has sufficient complementarity with the sequence of the strand to be amplified to hybridize therewith and form a template for synthesis of the extension product of the other primer.

[0027] The PCR primers for the signature region are based upon the highly conserved sequences of two or more aligned sequences (e.g., two or more AAV serotypes). The primers can accommodate less than exact identity among the two or more aligned AAV serotypes at the 5' end or in the middle. However, the sequences at the 3' end of the primers correspond to a region of two or more aligned AAV serotypes in which there is exact identity over at least five, preferably, over at least nine base pairs, and more preferably, over at least 18 base pairs at the 3' end of the primers. Thus, the 3' end of the primers is composed of sequences with 100% identity to the aligned sequences over at least five nucleotides. However, one can optionally utilize one, two, or more degenerate nucleotides at the 3' end of the primer.

[0028] For example, the primer set for the signature region of AAV was designed based upon a unique region within the AAV capsid, as follows. The 5' primer was based upon nt 2867-2891 of AAV2 [SEQ ID NO:7], 5'-GGTAATTCCTCCGGAATTGGCATT3'. The 3' primer was designed based upon nt 3096-3122 of AAV2 [SEQ ID NO:7], 5'-GACTCATCAACAACAAGTGGGGATTG-3'. However, one of skill in the art may have readily designed the primer set based upon the corresponding regions of AAV 1, AAV3, AAV4, AAV5, AAV6, or based upon the information provided herein, AAV7, AAV10, AAV11, AAV12, or another novel AAV. In addition, still other primer sets can be readily designed to amplify this signature region, using techniques known to those of skill in the art.

B. Isolation of Target Sequences

[0029] As described herein, the present invention uses a first primer set which specifically amplifies the signature region of the target sequence, e.g., an AAV serotype, in order to permit detection of the target. In a situation in which

further sequences are desired, e.g., if a novel AA V serotype is identified, the signature region may be extended. Thus, the invention may further utilize one or more additional primer sets.

[0030] Suitably, these primer sets are designed to include either the 5' or 3' primer of the first primer set and a second primer unique to the primer set, such that the primer set amplifies a region 5' or 3' to the signature region which anneals to either the 5' end or the 3' end of the signature region. For example, a first primer set is composed of a 5' primer, P1 and a 3' primer P2 to amplify the signature region. In order to extend the signature region on its 3' end, a second primer set is composed of primer P1 and a 3' primer P4, which amplifies the signature region and contiguous sequences downstream of the signature region. In order to extend the signature region on its 5' end, a third primer set is composed of a 5' primer, P5, and primer P2, such that the signature region and contiguous sequences upstream of the signature region are amplified. These extension steps are repeated (or performed at the same time), as needed or desired. Thereafter, the products results from these amplification steps are fused using conventional steps to produce an isolated sequence of the desired length.

[0031] The second and third primer sets are designed, as with the primer set for the signature region, to amplify a region having highly conserved sequences among the aligned sequences. Reference herein to the term "second" or "third" primer set is for each of discussion only, and without regard to the order in which these primers are added to the reaction mixture, or used for amplification. The region amplified by the second primer set is selected so that upon amplification it anneals at its 5' end to the 3' end of the signature region. Similarly, the region amplified by the third primer set is selected so that upon amplification it anneals at its 3' end to the 5' end of the signature region. Additional primer sets can be designed such that the regions which they amplify anneal to the either the 5' end or the 3' end of the extension products formed by the second or third primer sets, or by subsequent primer sets.

[0032] For example, where AAV is the target sequence, a first set of primers (P1 and P2) are used to amplify the signature region from the sample. In one desirable embodiment, this signature region is located within the AAV capsid. A second set of primers (P1 and P4) is used to extend the 3' end of the signature region to a location in the AAV sequence which is just before the AAV 3' ITR, i.e., providing an extension product containing the entire 3' end of the AAV capsid when using the signature region as an anchor. In one embodiment, the P4 primer corresponds to nt 4435 to 4462 of AAV2 [SEQ ID NO:7], and corresponding sequences in the other AAV serotypes. This results in amplification of a region of about 1.6 kb, which contains the 0.25 kb signature region. A third set of primers (P3 and P2) is used to extend the 5' end of signature region to a location in the AAV sequences which is in the 3' end of the rep genes, i.e., providing an extension product containing the entire 5' end of the AAV capsid when using the signature region as an anchor. In one embodiment, the P3 primer corresponds to nt 1384 to 1409 of AAV2 [SEQ ID NO:7], and corresponding sequences in the other AAV serotypes. This results in amplification of a region of about 1.7 kb, which contains the 0.25 kb signature region. Optionally, a fourth set of primers are used to further extend the extension product containing the entire 5' end of the AAV capsid to also include the rep sequences. In one embodiment, the primer designated P5 corresponds to nt 108 to 133 of AAV2 [SEQ ID NO:7], and corresponding sequences in the other AAV serotypes and is used in conjunction with the P2 primer.

[0033] Following completion of the desired number of extension steps, the various extension products are fused, making use of the signature region as an anchor or marker, to construct an intact sequence. In the example provided herein, AAV sequences containing, at a minimum, an intact AAV cap gene are obtained. Larger sequences may be obtained, depending upon the number of extension steps performed.

[0034] Suitably, the extension products are assembled into an intact AAV sequence using methods known to those of skill in the art. For example, the extension products may be digested with DralI, which cleaves at the DralI site located within the signature region, to provide restriction fragments which are re-ligated to provide products containing (at a minimum) an intact AAV cap gene. However, other suitable techniques for assembling the extension products into an intact sequence may be utilized. See, generally, Sambrook et al, cited herein.

[0035] As an alternative to the multiple extension steps described above, another embodiment of the invention provides for direct amplification of a 3.1 kb fragment which allows isolation of full-length cap sequences. To directly amplify a 3.1 kb full-length cap fragment from NHP tissue and blood DNAs, two other highly conserved regions were identified in AAV genomes for use in PCR amplification of large fragments. A primer within a conserved region located in the middle of the rep gene is utilized (AV1ns: 5' GCTGCGTCAACTGGACCAATGAGAAC 3', nt of SEQ ID NO:6) in combination with the 3' primer located in another conserved region downstream of the Cap gene (AV2cas: 5' CGCAGAGACCAAAGT-TCAACTGAAACGA 3', SEQ ID NO: 7) for amplification of AAV sequences including the full-length AAV cap. Typically, following amplification, the products are cloned and sequence analysis is performed with an accuracy of $\geq 99.9\%$. Using this method, the inventors have isolated at least 50 capsid clones which have subsequently been characterized. Among them, 37 clones were derived from Rhesus macaque tissues (rh.1 - rh.37), 6 clones from cynomolgous macaques (cy.1 - cy.6), 2 clones from Baboons (bb.1 and bb.2) and 5 clones from Chimps (ch.1 - ch.5). These clones are identified elsewhere in the specification, together with the species of animal from which they were identified and the tissues in that animal these novel sequences have been located.

II. Diagnostic Kit

[0036] In another aspect, the invention provides a diagnostic kit as defined in claim 23 hereinafter for detecting the presence of an unknown adeno-associated virus (AAV) in a sample. Such a kit may contain a first set of 5' and 3' PCR primers specific for a signature region of the AAV nucleic acid sequence. Alternatively, or additionally, such a kit can contain a first set of 5' and 3' PCR primers specific for the 3.1 kb fragment which includes the full-length AAV capsid nucleic acid sequence identified herein (e.g., the AV1ns and AV2cas primers.) Optionally, a kit of the invention may further contain two or more additional sets of 5' and 3' primers, as described herein, and/or PCR probes. These primers and probes are used according to the present invention to amplify signature regions of each AAV serotype, e.g., using quantitative PCR.

[0037] Such a kit may further include one or more restriction enzymes, standards for AAV serotypes providing their "signature restriction enzyme digestions analyses", and/or other means for determining the serotype of the AAV detected.

[0038] In addition, kits of the invention may include, instructions, a negative and/or positive control, containers, diluents and buffers for the sample, indicator charts for signature comparisons, disposable gloves, decontamination instructions, applicator sticks or containers, and sample preparator cups, as well as any desired reagents, including media, wash reagents and concentration reagents. Such reagents may be readily selected from among the reagents described herein, and from among conventional concentration reagents. In one desirable embodiment, the wash reagent is an isotonic saline solution which has been buffered to physiologic pH, such as phosphate buffered saline (PBS); the elution reagent is PBS containing 0.4 M NaCl, and the concentration reagents and devices. For example, one of skill in the art will recognize that reagents such as polyethylene glycol (PEG), or NH_4SO_4 may be useful, or that devices such as filter devices. For example, a filter device with a 100 K membrane would concentrate rAAV.

[0039] The kits provided by the present invention are useful for performing the methods described herein, and for study of biodistribution, epidemiology, mode of transmission of novel AAV serotypes in human and NHPs.

[0040] Thus, the methods and kits of the invention permit identification of target AAV sequences, particularly integrated AAV sequences.

[0041] In one notable example, the method of the invention facilitated analysis of cloned AAV sequences by the inventors, which revealed heterogeneity of proviral sequences between cloned fragments from different animals, all of which were distinct from the known six AAV serotypes, with the majority of the variation localized to hypervariable regions of the capsid protein. Surprising divergence of AAV sequences was noted in clones isolated from single tissue sources, such as lymph node, from an individual rhesus monkey. This heterogeneity is best explained by apparent evolution of AAV sequence within individual animals due, in part, to extensive homologous recombination between a limited number of co-infecting parenteral viruses. These studies suggest sequence evolution of widely disseminated virus during the course of a natural AAV infection that presumably leads to the formation of swarms of quasispecies which differ from one another in the array of capsid hypervariable regions. This is the first example of rapid molecular evolution of a DNA virus in a way that formerly was thought to be restricted to RNA viruses.

[0042] Sequences of several novel AAV serotypes identified by the method of the invention and characterization of these serotypes is provided.

III. Novel AAV Serotypes

A. Nucleic Acid Sequences

[0043] Nucleic acid sequences of novel AAV serotypes identified by the methods of the invention are provided. See, SEQ ID NO:1, 9 - 59, and 117 - 120. See also and the sequence listing.

[0044] For novel serotype AAV7, the full-length sequences, including the AAV 5' ITRs, capsid, rep, and AAV 3' ITRs are provided in SEQ ID NO:1.

[0045] For other novel AAV serotypes, the approximately 3.1 kb fragment isolated according to the method of the invention is provided. This fragment contains sequences encoding full-length capsid protein and all or part of the sequences encoding the rep protein. These sequences include the clones identified below.

[0046] For still other novel AAV serotypes, the signature region encoding the capsid protein is provided. For example, the AAV10 nucleic acid sequences include those illustrated in See, SEQ ID NO:117, which spans 255 bases. The AAV11 nucleic acid sequences include the DNA sequences illustrated in SEQ ID NO:118 which spans 258 bases. The AAV12 nucleic acid sequences include the DNA sequences illustrated in SEQ ID NO: 119, which consists of 255 bases. Using the methodology described above, further AAV10, AAV11 and AAV 12 sequences can be readily identified and used for a variety of purposes, including those described for AAV7 and the other novel serotypes herein.

[0047] Novel NHP sequences identified by the invention include those provided in the following Table I, which are identified by clone number:

Table 1

AAV Cap Sequence	Clone Number	Source		
		Species	Tissue	SEQ ID NO (DNA)
Rh.1	Clone 9 (AAV9)	Rhesus	Heart	5
Rh.2	Clone 43.1	Rhesus	MLN	39
Rh.3	Clone 43.5	Rhesus	MLN	40
Rh.4	Clone 43.12	Rhesus	MLN	41
Rh.5	Clone 43.20	Rhesus	MLN	42
Rh.6	Clone 43.21	Rhesus	MLN	43
Rh.7	Clone 43.23	Rhesus	MLN	44

Table 1 (cont'd)

Rh.8	Clone 43.25	Rhesus	MLN	45
Rh.9	Clone 44.1	Rhesus	Liver	46
Rh.10	Clone 44.2	Rhesus	Liver	59
Rh.11	Clone 44.5	Rhesus	Liver	47
Rh.12	Clone 42.1B	Rhesus	MLN	30
Rh.13	42.2	Rhesus	MLN	9
Rh.14	Clone 42.3A	Rhesus	MLN	32
Rh.15	Clone 42.3B	Rhesus	MLN	36
Rh.16	Clone 42.4	Rhesus	MLN	33
Rh.17	Clone 42.5A	Rhesus	MLN	34
Rh.18	Clone 42.5B	Rhesus	MLN	29
Rh.19	Clone 42.6B	Rhesus	MLN	38
Rh.20	Clone 42.8	Rhesus	MLN	27
Rh.21	Clone 42.10	Rhesus	MLN	35
Rh.22	Clone 42.11	Rhesus	MLN	37
Rh.23	Clone 42.12	Rhesus	MLN	58
Rh.24	Clone 42.13	Rhesus	MLN	31
Rh.25	Clone 42.15	Rhesus	MLN	28
Rh.26	Clone 223.2	Rhesus	Liver	49
Rh.27	Clone 223.4	Rhesus	Liver	50
Rh.28	Clone 223.5	Rhesus	Liver	51
Rh.29	Clone 223.6	Rhesus	Liver	52
Rh.30	Clone 223.7	Rhesus	Liver	53
Rh.31	Clone 223.10	Rhesus	Liver	48
Rh.32	Clone C1	Rhesus	Spleen, Duo, Kid & Liver	19
Rh.33	Clone C3	Rhesus		20
Rh.34	Clone C5	Rhesus		21
Rh.35	Clone F1	Rhesus	Liver	22
Rh.36	Clone F3	Rhesus		23
Rh.37	Clone F5	Rhesus		24
Cy.1	Clone 1.3	Cyno	Blood	14
Cy.2	Clone 13.3B	Cyno	Blood	15
Cy.3	Clone 24.1	Cyno	Blood	16
Cy.4	Clone 27.3	Cyno	Blood	17
Cy.5	Clone 7.2	Cyno	Blood	18
Cy.6	Clone 16.3	Cyno	Blood	10

Table 1 (cont'd)

bb.1	Clone 29.3	Baboon	Blood	11
bb.2	Clone 29.5	Baboon	Blood	13
Ch.1	Clone A3.3	Chimp	Blood	57
Ch.2	Clone A3.4	Chimp	Blood	54
Ch.3	Clone A3.5	Chimp	Blood	55
Ch.4	Clone A3.7	Chimp	Blood	56

[0048] A novel NHP clone was made by splicing capsids fragments of two chimp adenoviruses into an AAV2 rep construct. This new clone, A3.1, is also termed Ch.5 [SEQ ID NO:20]. Additionally, the present invention includes two human AAV sequences, termed H6 [SEQ ID NO:25] and H2 [SEQ ID NO:26].

[0049] The AAV nucleic acid sequences further encompass the strand which is complementary to the strands provided in the sequences provided in the Sequence Listing [SEQ ID NO:1, 9 - 59, 117-120], nucleic acid sequences, as well as the RNA and cDNA sequences corresponding to the sequences provided in the Sequence Listing [SEQ ID NO:1, 9 - 59, 117-120], and their complementary strands. Also included in the nucleic acid sequences are natural variants and engineered modifications of the sequences of the Sequence Listing [SEQ ID NO:1, 9 - 59, 117-120], and their complementary strands. Such modifications include, for example, labels which are known in the art, methylation, and substitution of one or more of the naturally occurring nucleotides with a degenerate nucleotide.

[0050] Further included are nucleic acid sequences which are greater than 85%, preferably at least about 90%, more preferably at least about 95%, and most preferably at least about 98 to 99% identical or homologous to the sequences of the invention, including the Sequence Listing [SEQ ID NO:1, 9 - 59, 117-120]. These terms are as defined herein.

[0051] Also included are fragments of the novel AAV sequences identified by the method described herein. Suitable fragments are at least 15 nucleotides in length, and encompass functional fragments, i.e., fragments which are of biological interest. In one embodiment, these fragments are fragments of the novel sequences of the Sequence Listing [SEQ ID NO:1, 9 - 59, 117-120], their complementary strands, cDNA and RNA complementary thereto.

[0052] Examples of suitable fragments are provided with respect to the location of these fragments on AAV1, AAV2, or AAV7. However, using the alignment provided herein (obtained using the Clustal W program at default settings), or similar techniques for generating an alignment with other novel serotypes of the invention, one of skill in the art can readily identify the precise nucleotide start and stop codons for desired fragments.

[0053] Examples of suitable fragments include the sequences encoding the three variable proteins (vp) of the AAV capsid which are alternative splice variants: vp1 [e.g., nt 825 to 3049 of AAV7, SEQ ID NO: 1]; vp2 [e.g., nt 1234 - 3049 of AAV7, SEQ ID NO: 1]; and vp 3 [e.g., nt 1434 - 3049 of AAV7, SEQ ID NO:1]. It is notable that AAV7 has an unusual GTG start codon. With the exception of a few house-keeping genes, such a start codon has not previously been reported in DNA viruses. The start codons for vp1, vp2 and vp3 for other AAV serotypes have been believed to be such that they permit the cellular mechanism of the host cell in which they reside to produce vp1, vp2 and vp3 in a ratio of 10%:10%:80%, respectively, in order to permit efficient assembly of the virion. However, the AAV7 virion has been found to assemble efficiently even with this rare GTG start codon. Thus, the inventors anticipate this it is desirable to alter the start codon of the vp3 of other AAV serotypes to contain this rare GTG start codon, in order to improve packaging efficiency, to alter the virion structure and/or to alter location of epitopes (e.g., neutralizing antibody epitopes) of other AAV serotypes. The start codons may be altered using conventional techniques including, e.g., site directed mutagenesis. The altered AAV virions may be of any selected serotype, composed of a vp 3, and/or optionally, vp 1 and/or vp2 having start codons altered to GTG.

[0054] Other suitable fragments of AAV, include a fragment containing the start codon for the AAV capsid protein [e.g., nt 468 to 3090 of AAV7, SEQ ID NO:1, nt 725 to 3090 of AAV7, SEQ ID NO: 1, and corresponding regions of the other AAV serotypes]. Still other fragments of AAV7 and the other novel AAV serotypes identified using the methods described herein include those encoding the rep proteins, including *rep* 78 [e.g., initiation codon 334 for AAV7], *rep* 68 [initiation codon nt 334 for AAV7], *rep* 52 [initiation codon 1006 for AAV7], and *rep* 40 [initiation codon 1006 for AAV7]. Other fragments of interest may include the AAV 5' inverted terminal repeats ITRs, [nt 1 to 107 for AAV7]; the AAV 3' ITRs [nt 4704 to 4721 for AAV7], P19 sequences, AAV P40 sequences, the rep binding site, and the terminal resolution site (TRS). Still other suitable fragments will be readily apparent to those of skill in the art.

[0055] In addition to the nucleic acid sequences provided in the figures and Sequence Listing, there are nucleic acid molecules and sequences which are designed to express the amino acid sequences, proteins and peptides of the AAV serotypes of the invention. These include nucleic acid sequences which encode the following novel AAV amino acid sequences: C1 [SEQ ID NO:60], C2 [SEQ ID NO:61], C5 [SEQ ID NO:62], A3-3 [SEQ ID NO:66], A3-7 [SEQ ID NO:67],

A3-4 [SEQ ID NO:68], A3-5 [SEQ ID NO: 69], 3.3b [SEQ ID NO: 62], 223.4 [SEQ ID NO: 73], 223-5 [SEQ ID NO:74], 223-10 [SEQ ID NO:75], 223-2 [SEQ ID NO:76], 223-7 [SEQ ID NO: 77], 223-6 [SEQ ID NO: 78], 44-1 [SEQ ID NO: 79], 44-5 [SEQ ID NO:80], 44-2 [SEQ ID NO:81], 42-15 [SEQ ID NO: 84], 42-8 [SEQ ID NO: 85], 42-13 [SEQ ID NO:86], 42-3A [SEQ ID NO:87], 42-4 [SEQ ID NO:88], 42-5A [SEQ ID NO:89], 42-1B [SEQ ID NO:90], 42-5B [SEQ ID NO:91], 43-1 [SEQ ID NO: 92], 43-12 [SEQ ID NO: 93], 43-5 [SEQ ID NO:94], 43-21 [SEQ ID NO:96], 43-25 [SEQ ID NO: 97], 43-20 [SEQ ID NO:99], 24.1 [SEQ ID NO: 101], 42.2 [SEQ ID NO:102], 7.2 [SEQ ID NO: 103], 27.3 [SEQ ID NO: 104], 16.3 [SEQ ID NO: 105], 42.10 [SEQ ID NO: 106], 42-38 [SEQ ID NO: 107], 42-11 [SEQ ID NO: 108], F1 [SEQ ID NO: 109], F5 [SEQ ID NO: 110], F3 [SEQ ID NO:111], 42-6B [SEQ ID NO: 112], and/or 42-12 [SEQ ID NO: 113], and artificial AAV serotypes generated using these sequences and/or unique fragments thereof.

[0056] As used herein, artificial AAV serotypes include, without limitation, AAV with a non-naturally occurring capsid protein. Such an artificial capsid may be generated by any suitable technique, using a novel AAV sequence (e.g., a fragment of a vp1 capsid protein) in combination with heterologous sequences which may be obtained from another AAV serotype (known or novel), non-contiguous portions of the same AAV serotype, from a non-AAV viral source, or from a non-viral source. An artificial AAV serotype may be, without limitation, a chimeric AAV capsid, a recombinant AAV capsid, or a "humanized" AAV capsid.

B. AAV Amino Acid Sequences, Proteins and Peptides

[0057] The invention provides proteins and fragments thereof which are encoded by the nucleic acid sequences of the novel AAV serotypes identified herein, including, e.g., AA V7 [nt 825 to 3049 of AA V7, SEQ ID NO: 1] the other novel serotypes provided herein. Thus, the capsid proteins of the novel serotypes of the invention, including: H6 [SEQ ID NO: 25], H2 [SEQ ID NO: 26], 42-2 [SEQ ID NO:9], 42-8 [SEQ ID NO:27], 42-15 [SEQ ID NO:28], 42-5b [SEQ ID NO: 29], 42-1b [SEQ ID NO:30], 42-13 [SEQ ID NO: 31], 42-3a [SEQ ID NO: 32], 42-4 [SEQ ID NO:33], 42-5a [SEQ ID NO: 34], 42-10 [SEQ ID NO:35], 42-3b [SEQ ID NO: 36], 42-11 [SEQ ID NO: 37], 42-6b [SEQ ID NO:38], 43-1 [SEQ ID NO: 39], 43-5 [SEQ ID NO: 40], 43-12 [SEQ ID NO:41], 43-20 [SEQ ID NO:42], 43-21 [SEQ ID NO: 43], 43-23 [SEQ ID NO:44], 43-25 [SEQ ID NO: 45], 44.1 [SEQ ID NO:47], 44.5 [SEQ ID NO:47], 223.10 [SEQ ID NO:48], 223.2 [SEQ ID NO:49], 223.4 [SEQ ID NO:50], 223.5 [SEQ ID NO:51], 223.6 [SEQ ID NO: 52], 223.7 [SEQ ID NO: 53], A3.4 [SEQ ID NO: 54], A3.5 [SEQ ID NO:55], A3.7 [SEQ ID NO: 56], A3.3 [SEQ ID NO:57], 42.12 [SEQ ID NO: 58], and 44.2 [SEQ ID NO: 59], can be readily generated using conventional techniques from the open reading frames provided for the above-listed clones.

[0058] The sequences, proteins, and fragments may be produced by any suitable means, including recombinant production, chemical synthesis, or other synthetic means. Such production methods are within the knowledge of those of skill in the art.

IV. Production of rAAV with novel AAV capsids

[0059] Novel, wild-type AAV serotypes can be identified by the invention, the sequences of which wild-type AAV serotypes are free of DNA and/or cellular material with these viruses are associated in nature. In another aspect, the present invention provides molecules which utilize the novel AAV sequences of the invention, including fragments thereof, for production of molecules useful in delivery of a heterologous gene or other nucleic acid sequences to a target cell.

[0060] The following examples illustrate several aspects and embodiments of the invention.

EXAMPLES

Example 1: PCR amplification, cloning and characterization of novel AAV sequences.

[0061] Tissues from nonhuman primates were screened for AAV sequences using a PCR method based on oligonucleotides to highly conserved regions of known AAVs. A stretch of AAV sequence spanning 2886 to 3143 bp of AAV1 [SEQ ID NO:6] was selected as a PCR amplicon in which a hypervariable region of the capsid protein (Cap) that is unique to each known AAV serotype, which is termed herein a "signature region," is flanked by conserved sequences. In later analysis, this signature region was shown to be located between conserved residues spanning hypervariable region 3.

[0062] An initial survey of peripheral blood of a number of nonhuman primate species revealed detectable AAV in a subset of animals from species such as rhesus macaques, cynomolgous macaques, chimpanzees and baboons. However, there were no AAV sequences detected in some other species tested, including Japanese macaques, pig-tailed macaques and squirrel monkeys. A more extensive analysis of vector distribution was conducted in tissues of rhesus monkeys of the University of Pennsylvania and Tulane colonies recovered at necropsy. This revealed AAV sequence throughout a wide array of tissues.

A. Amplification of an AAV signature region

[0063] DNA sequences of AAV1-6 and AAVs isolated from Goose and Duck were aligned to each other using "Clustal W" at default settings. Sequence similarities among AAVs were compared.

[0064] In the line of study, a 257 bp region spanning 2886 bp to 3143 bp of AAV 1 [SEQ ID NO: 6], and the corresponding region in the genomes of AAV 2-6 genomes was identified by the inventors. This region is located with the AAV capsid gene and has highly conserved sequences among at both 5' and 3' ends and is relatively variable sequence in the middle. In addition, this region contains a *DraIII* restriction enzyme site (CACCACGTC, SEQ ID NO:15). The inventors have found that this region serves as specific signature for each known type of AAV DNA. In other words, following PCR reactions, digestion with endonucleases that are specific to each known serotypes and gel electrophoresis analysis, this regions can be used to definitively identify amplified DNA as being from serotype 1, 2, 3, 4, 5, 6, or another serotype.

[0065] The primers were designed, validated and PCR conditions optimized with AAV1, 2 and 5 DNA controls. The primers were based upon the sequences of AAV2: 5' primer, 1S: bp 2867-2891 of AAV2 (SEQ ID NO:7) and 3' primer, 18as, bp 3095-3121 of AAV2 (SEQ ID NO:7).

[0066] Cellular DNAs from different tissues including blood, brain, liver, lung, testis, etc. of different rhesus monkeys were studied utilizing the strategy described above. The results revealed that DNAs from different tissues of these monkeys gave rise to strong PCR amplifications. Further restriction analyses of PCR products indicated that they were amplified from AAV sequences different from any published AAV sequences.

[0067] PCR products (about 255 bp in size) from DNAs of a variety of monkey tissues have been cloned and sequenced. Bioinformatics study of these novel AAV sequences indicated that they are novel AAV sequences of capsid gene and distinct from each other. Multiple sequence alignment analysis was performed using the Clustal W (1.81) program. The percentage of sequence identity between the signature regions of AAV 1-7 and AAV 10-12 genomes is provided below.

Table 1. Sequences for Analysis

Sequence #	AAV Serotype	Size (bp)
1	AAV1	258
2	AAV2	255
3	AAV3	255
4	AAV4	246
5	AAV5	258
6	AAV6	258
7	AAV7	258
10	AAV10	255
11	AAV11	258
12	AAV12	255

Table 3. Pairwise Alignment (Percentage of Identity)

	AAV2	AAV3	AAV4	AAV5	AAV6	AAV7	AAV10	AAV11	AAV12
AAV1	90	90	81	76	97	91	93	94	93
AAV2		93	79	78	90	90	93	93	92
AAV3			80	76	90	92	92	92	92
AAV4				76	81	84	82	81	79
AAV5					75	78	79	79	76
AAV6						91	92	94	94
AAV7							94	92	92
AAV10								95	93

Table continued

	AAV2	AAV3	AAV4	AAV5	AAV6	AAV7	AAV10	AAV11	AAV12
AAV11									94

[0068] Over 300 clones containing novel AAV serotype sequences that span the selected 257 bp region were isolated and sequenced. Bioinformatics analysis of these 300+ clones suggests that this 257 bp region is critical in serving as a good land marker or signature sequence for quick isolation and identification of novel AAV serotype.

B. Use of the signature region for PCR amplification.

[0069] The 257 bp signature region was used as a PCR anchor to extend PCR amplifications to 5' of the genome to cover the junction region of rep and cap genes (1398 bp - 3143 bp, SEQ ID NO:6) and 3' of the genome to obtain the entire cap gene sequence (2866 bp - 4600 bp, SEQ ID NO:6). PCR amplifications were carried out using the standard conditions, including denaturing at 95°C for 0.5-1 min, annealing at 60-65°C for 0.5-1 min and extension at 72°C for 1 min per kb with a total number of amplification cycles ranging from 28 to 42.

[0070] Using the aligned sequences as described in "A", two other relative conserved regions were identified in the sequence located in 3' end of rep genes and 5' to the 257 bp region and in the sequence down stream of the 257 bp fragment but before the AAV' 3 ITR. Two sets of new primers were designed and PCR conditions optimized for recovery of entire capsid and a part of rep sequences of novel AAV serotypes. More specifically, for the 5' amplification, the 5' primer, AV1Ns, was GCTGCGTCAACTGGACCAATGAGAAC [nt 1398-1423 of AAV1, SEQ ID NO:6] and the 3' primer was 18as, identified above. For the 3' amplification, the 5' primer was 1s, identified above, and the 3' primer was AV2Las, TCGTTTCAGTTGAACCTTGGTCTCTGCG [nt 4435-4462 of AAV2, SEQ ID NO:7].

[0071] In these PCR amplifications, the 257 bp region was used as a PCR anchor and land marker to generate overlapping fragments to construct a complete capsid gene by fusion at the DraIII site in the signature region following amplification of the 5' and 3' extension fragments obtained as described herein. More particularly, to generate the intact AAV7 cap gene, the three amplification products (a) the sequences of the signature region; (b) the sequences of the 5' extension; and (c) the sequences of the 3' extension were cloned into a pCR4-Topo [Invitrogen] plasmid backbone according to manufacturer's instructions. Thereafter, the plasmids were digested with DraIII and recombined to form an intact cap gene.

[0072] In this line of work, about 80 % of capsid sequences of AAV7 and AAV 8 were isolated and analyzed. Another novel serotype, AAV9, was also discovered from Monkey #2.

[0073] Using the PCR conditions described above, the remaining portion of the rep gene sequence for AAV7 is isolated and cloned using the primers that amplify 108 bp to 1461 bp of AAV genome (calculated based on the numbering of AAV2, SEQ ID NO:7). This clone is sequenced for construction of a complete AAV7 genome without ITRs.

C. Direct Amplification of 3.1 kb Cap fragment

[0074] To directly amplify a 3.1 kb full-length Cap fragment from NHP tissue and blood DNAs, two other highly conserved regions were identified in AAV genomes for use in PCR amplification of large fragments. A primer within a conserved region located in the middle of the rep gene was selected (AV1ns: 5' GCTGCGTCAACTGGACCAATGAGAAC 3', nt 1398-1423 of SEQ ID NO:6) in combination with the 3' primer located in another conserved region downstream of the Cap gene (AV2cas: 5' CGCAGAGACCAAAGTTCAACTGAAACGA 3', SEQ ID NO:7) for amplification of full-length cap fragments. The PCR products were Topo-cloned according to manufacturer's directions (Invitrogen) and sequence analysis was performed by Qiagen Genomics (Qiagen Genomics, Seattle, WA) with an accuracy of ≥ 99.9%. A total of 50 capsid clones were isolated and characterized. Among them, 37 clones were derived from Rhesus macaque tissues (rh.1 - rh.37), 6 clones from cynomolgous macaques (cy.1 - cy.6), 2 clones from Baboons (bb.1 and bb.2) and 5 clones from Chimps (ch.1 - ch.5).

[0075] To rule out the possibility that sequence diversity within the novel AAV family was not an artifact of the PCR, such as PCR-mediated gene splicing by overlap extension between different partial DNA templates with homologous sequences, or the result of recombination process in bacteria, a series of experiments were performed under identical conditions for VP1 amplification using total cellular DNAs. First, intact AAV7 and AAV8 plasmids were mixed at an equal molar ratio followed by serial dilutions. The serially diluted mixtures were used as templates for PCR amplification of 3.1 kb VP1 fragments using universal primers and identical PCR conditions to that were used for DNA amplifications to see whether any hybrid PCR products were generated. The mixture was transformed into bacteria and isolated transformants to look for hybrid clones possibly derived from recombination process in bacterial cells. In a different experiment, we restricted AAV7 and AAV8 plasmids with Msp I, Ava I and HaeI, all of which cut both genomes multiple times at different

positions, mixed the digestions in different combinations and used them for PCR amplification of VP1 fragments under the same conditions to test whether any PCR products could be generated through overlap sequence extension of partial AAV sequences. In another experiment, a mixture of gel purified 5' 1.5 kb AAV7 VP1 fragment and 3' 1.7 kb AAV8 VP1 fragment with overlap in the signature region was serially diluted and used for PCR amplification in the presence and absence of 200 ng cellular DNA extracted from a monkey cell line that was free of AAV sequences by TaqMan analysis. None of these experiments demonstrated efficient PCR-mediated overlap sequence production under the conditions of the genomic DNA Cap amplification (data not shown). As a further confirmation, 3 pairs of primers were designed, which were located at different HVRs, and were sequence specific to the variants of clone 42s from Rhesus macaque F953, in different combinations to amplify shorter fragments from mesenteric lymph node (MLN) DNA from F953 from which clone 42s were isolated. All sequence variations identified in full-length Cap clones were found in these short fragments (data not shown).

Example 2: Adeno-Associated Viruses Undergo Substantial Evolution in Primates During Natural Infections

[0076] Sequence analysis of selected AAV isolates revealed divergence throughout the genome that is most concentrated in hypervariable regions of the capsid proteins. Epidemiologic data indicate that all known serotypes are endemic to primates, although isolation of clinical isolates has been restricted to AAV2 and AAV3 from anal and throat swabs of human infants and AAV5 from a human condylomatous wart. No known clinical sequelae have been associated with AAV infection.

[0077] In an attempt to better understand the biology of AAV, nonhuman primates were used as models to characterize the sequelae of natural infections. Tissues from nonhuman primates were screened for AAV sequences using the PCR method of the invention based on oligonucleotides to highly conserved regions of known AAVs (see Example 1). A stretch of AAV sequence spanning 2886 to 3143 bp of AAV1 [SEQ ID NO:6] was selected as a PCR amplicon in which conserved sequences are flanked by a hypervariable region that is unique to each known AAV serotype, termed herein a "signature region."

[0078] An initial survey of peripheral blood of a number of nonhuman primate species including rhesus monkeys, cynomolgous monkeys, chimpanzees, and baboons revealed detectable AAV in a subset of animals from all species. A more extensive analysis of vector distribution was conducted in tissues of rhesus monkeys of the University of Pennsylvania and Tulane colonies recovered at necropsy. This revealed AAV sequence throughout a wide array of tissues.

[0079] The amplified signature sequences were subcloned into plasmids and individual transformants were subjected to sequence analysis. This revealed substantial variation in nucleotide sequence of clones derived from different animals. Variation in the signature sequence was also noted in clones obtained within individual animals. Tissues harvested from two animals in which unique signature sequences were identified (i.e., colon from 98E044 and heart from 98E056) were further characterized by expanding the sequence amplified by PCR using oligonucleotides to highly conserved sequences. In this way, complete proviral structures were reconstructed for viral genomes from both tissues as described herein. These proviruses differ from the other known AAVs with the greatest sequence divergence noted in regions of the Cap gene.

[0080] Additional experiments were performed to confirm that AAV sequences resident to the nonhuman primate tissue represented proviral genomes of infectious virus that is capable of being rescued and form virions. Genomic DNA from liver tissue of animal 98E056, from which AAV8 signature sequence was detected, was digested with an endonuclease that does not have a site within the AAV sequence and transfected into 293 cells with a plasmid containing an E1 deleted genome of human adenovirus serotype 5 as a source of helper functions. The resulting lysate was passaged on 293 cells once and the lysate was recovered and analyzed for the presence of AAV Cap proteins using a broadly reacting polyclonal antibody to Cap proteins and for the presence and abundance of DNA sequences from the PCR amplified AAV provirus from which AAV8 was derived. Transfection of endonuclease restricted heart DNA and the adenovirus helper plasmid yielded high quantities of AAV8 virus as demonstrated by the detection of Cap proteins by Western blot analysis and the presence of 10^4 AAV8 vector genomes per 293 cell. Lysates were generated from a large-scale preparation and the AAV was purified by cesium sedimentation. The purified preparation demonstrated 26 nm icosahedral structures that look identical to those of AAV serotype 2. Transfection with the adenovirus helper alone did not yield AAV proteins or genomes, ruling out contamination as a source of the rescued AAV.

[0081] To further characterize the inter and intra animal variation of AAV signature sequence, selected tissues were subjected to extended PCR to amplify entire Cap open reading frames.

[0082] The resulting fragments were cloned into bacterial plasmids and individual transformants were isolated and fully sequenced. This analysis involved mesenteric lymph nodes from three rhesus monkeys (Tulane/V223 - 6 clones; Tulane/T612 - 7 clones; Tulane/F953 - 14 clones), liver from two rhesus monkeys (Tulane/V251 - 3 clones; Penn/00E033 - 3 clones), spleen from one rhesus monkey (Penn/97E043 - 3 clones), heart from one rhesus monkey (IHGT/98E046 - 1 clone) and peripheral blood from one chimpanzee (New Iberia/X133 - 5 clones), six cynomolgous macaques (Charles River/A1378, A3099, A3388, A3442, A2821, A3242 - 6 clones total) and one Baboon (SFRB/8644 - 2 clones). Of the

50 clones that were sequenced from 15 different animals, 30 were considered non-redundant based on the finding of at least 7 amino acid differences from one another. The non-redundant VP1 clones are numbered sequentially as they were isolated, with a prefix indicating the species of non-human primate from which they were derived. The structural relationships between these 30 non-redundant clones and the previously described 8 AAV serotypes were determined using the SplitsTree program [Huson, D. H. SplitsTree: analyzing and visualizing evolutionary data. *Bioinformatics* **14**, 68-73 (1998)] with implementation of the method of split decomposition. The analysis depicts homoplasy between a set of sequences in a tree-like network rather than a bifurcating tree. The advantage is to enable detection of groupings that are the result of convergence and to exhibit phylogenetic relationships even when they are distorted by parallel events. Extensive phylogenetic research will be required in order to elucidate the AAV evolution, whereas the intention here only is to group the different clones as to their sequence similarity.

[0083] To confirm that the novel VP1 sequences were derived from infectious viral genomes, cellular DNA from tissues with high abundance of viral DNA was restricted with an endonuclease that should not cleave within AAV and transfected into 293 cells, followed by infection with adenovirus. This resulted in rescue and amplification of AAV genomes from DNA of tissues from two different animals (data not shown).

[0084] VP1 sequences of the novel AAVs were further characterized with respect to the nature and location of amino acid sequence variation. All 30 VP1 clones that were shown to differ from one another by greater than 1% amino acid sequence were aligned and scored for variation at each residue. An algorithm developed to determine areas of sequence divergence yielded 12 hypervariable regions (HVR) of which 5 overlap or are part of the 4 previously described variable regions [Kotin, cited above; Rutledge, cited above]. The threefold-proximal peaks contain most of the variability (HVR5-10). Interestingly the loops located at the 2 and 5 fold axis show intense variation as well. The HVRs 1 and 2 occur in the N-terminal portion of the capsid protein that is not resolved in the X-ray structure suggesting that the N-terminus of the VP1 protein is exposed on the surface of the virion.

[0085] Real-time PCR was used to quantify AAV sequences from tissues of 21 rhesus monkeys using primers and probes to highly conserved regions of Rep (one set) and Cap (two sets) of known AAVs. Each data point represents analysis from tissue DNA from an individual animal. This confirmed the wide distribution of AAV sequences, although the quantitative distribution differed between individual animals. The source of animals and previous history or treatments did not appear to influence distribution of AAV sequences in rhesus macaques. The three different sets of primers and probes used to quantify AAV yielded consistent results. The highest levels of AAV were found consistently in mesenteric lymph nodes at an average of 0.01 copies per diploid genome for 13 animals that were positive. Liver and spleen also contained high abundance of virus DNA. There were examples of very high AAV, such as in heart of rhesus macaque 98E056, spleen of rhesus macaque 97E043 and liver of rhesus macaque RQ4407, which demonstrated 1.5, 3 and 20 copies of AAV sequence per diploid genome respectively. Relatively low levels of virus DNA were noted in peripheral blood mononuclear cells, suggesting the data in tissue are not due to resident blood components (data not shown). It should be noted that this method would not necessarily capture all AAVs resident to the nonhuman primates since detection requires high homology to both the oligonucleotides and the real time PCR probe. Tissues from animals with high abundance AAV DNA was further analyzed for the molecular state of the DNA, by DNA hybridization techniques, and its cellular distribution, by *in situ* hybridization.

[0086] The kind of sequence variation revealed in AAV proviral fragments isolated from different animals and within tissues of the same animals is reminiscent of the evolution that occurs for many RNA viruses during pandemics or even within the infection of an individual. In some situations the notion of a wild-type virus has been replaced by the existence of swarms of quasispecies that evolve as a result of rapid replication and mutations in the presence of selective pressure. One example is infection by HIV, which evolves in response to immunologic and pharmacologic pressure. Several mechanisms contribute to the high rate of mutations in RNA viruses, including low fidelity and lack of proof reading capacity of reverse transcriptase and non-homologous and homologous recombination.

[0087] Evidence for the formation of quasispecies of AAV was illustrated in this study by the systematic sequencing of multiple cloned proviral fragments. In fact, identical sequences could not be found within any extended clones isolated between or within animals. An important mechanism for this evolution of sequence appears to be a high rate of homologous recombination between a more limited number of parenteral viruses. The net result is extensive swapping of hypervariable regions of the Cap protein leading to an array of chimeras that could have different tropisms and serologic specificities (i.e., the ability to escape immunologic responses especially as it relates to neutralizing antibodies). Mechanisms by which homologous recombination could occur are unclear. One possibility is that + and - strands of different single stranded AAV genomes anneal during replication as has been described during high multiplicity of infections with AAV recombinants. It is unclear if other mechanisms contribute to sequence evolution in AAV infections. The overall rate of mutation that occurs during AAV replication appears to be relatively low and the data do not suggest high frequencies of replication errors. However, substantial rearrangements of the AAV genome have been described during lytic infection leading to the formation of defective interfering particles. Irrespective of the mechanisms that lead to sequence divergence, with few exceptions, vp1 structures of the quasispecies remained intact without frameshifts or nonsense mutations suggesting that competitive selection of viruses with the most favorable profile of fitness contribute to the population

dynamics.

[0088] These studies have implications in several areas of biology and medicine. The concept of rapid virus evolution, formerly thought to be a property restricted to RNA viruses, should be considered in DNA viruses, which classically have been characterized by serologic assays. It will be important in terms of parvoviruses to develop a new method for describing virus isolates that captures the complexity of its structure and biology, such as with HIV, which are categorized as general families of similar structure and function called Clades. An alternative strategy is to continue to categorize isolates with respect to serologic specificity and develop criteria for describing variants within serologic groups.

Example 3: Vectorology of recombinant AAV genomes equipped with AAV2 ITRs using chimeric plasmids containing AAV2 rep and novel AAV cap genes for serological and gene transfer studies in different animal models.

[0089] Chimeric packaging constructs are generated by fusing AAV2 rep with cap sequences of novel AAV serotypes. These chimeric packaging constructs are used, initially, for pseudotyping recombinant AAV genomes carrying AAV2 ITRs by triple transfection in 293 cell using Ad5 helper plasmid. These pseudotyped vectors are used to evaluate performance in transduction-based serological studies and evaluate gene transfer efficiency of novel AAV serotypes in different animal models including NHP and rodents, before intact and infectious viruses of these novel serotypes are isolated.

A. *pAAV2GFP*

[0090] The AAV2 plasmid which contains the AAV2 ITRs and green fluorescent protein expressed under the control of a constitutive promoter. This plasmid contains the following elements: the AAV2 ITRs, a CMV promoter, and the GFP coding sequences.

B. *Cloning of trans plasmid*

[0091] To construct the chimeric trans-plasmid for production of recombinant pseudotyped AAV7 vectors, p5E18 plasmid (Xiao *et al.*, 1999, *J. Virol* **73**:3994-4003) was partially digested with Xho I to linearize the plasmid at the Xho I site at the position of 3169 bp only. The Xho I cut ends were then filled in and ligated back. This modified p5E18 plasmid was restricted with Xba I and Xho I in a complete digestion to remove the AAV2 cap gene sequence and replaced with a 2267 bp Spe I/Xho I fragment containing the AAV7 cap gene which was isolated from pCRAAV7 6-5+15-4 plasmid.

[0092] The resulting plasmid contains the AAV2 rep sequences for Rep78/68 under the control of the AAV2 P5 promoter, and the AAV2 rep sequences for Rep52/40 under the control of the AAV2 P19 promoter. The AAV7 capsid sequences are under the control of the AAV2 P40 promoter, which is located within the Rep sequences. This plasmid further contains a spacer 5' of the rep ORF.

C. *Production of Pseudotyped rAAV*

[0093] The rAAV particles (AAV2 vector in AAV7 capsid) are generated using an adenovirus-free method. Briefly, the cis plasmid (pAAV2.1 lacZ plasmid containing AAV2 ITRs), and the trans plasmid pCRAAV7 6-5+15-4 (containing the AAV2 rep and AAV7 cap) and a helper plasmid, respectively, were simultaneously co-transfected into 293 cells in a ratio of 1:1:2 by calcium phosphate precipitation.

[0094] For the construction of the pAd helper plasmids, pBG 10 plasmid was purchased from Microbix (Canada). A RsrII fragment containing L2 and L3 was deleted from pBHG10, resulting in the first helper plasmid, pAdΔF13. Plasmid AdΔ F1 was constructed by cloning Asp700/Sall fragment with a PmeI/Sgfl deletion, isolating from pBHG10, into Blue-script. MLP, L2, L2 and L3 were deleted in the pAdΔF1. Further deletions of a 2.3 kb NruI fragment and, subsequently, a 0.5 kb RsrII/NruI fragment generated helper plasmids pAdΔF5 and pAdΔF6, respectively. The helper plasmid, termed pΔF6, provides the essential helper functions of E2a and E4 ORF6 not provided by the E1-expressing helper cell, but is deleted of adenoviral capsid proteins and functional E1 regions).

[0095] Typically, 50 μg of DNA (cis:trans:helper) was transfected onto a 150 mm tissue culture dish. The 293 cells were harvested 72 hours post-transfection, sonicated and treated with 0.5% sodium deoxycholate (37°C for 10 min.) Cell lysates were then subjected to two rounds of a CsCl gradient. Peak fractions containing rAAV vector are collected, pooled and dialyzed against PBS.

Example 4: Creation of infectious clones carrying intact novel AAV serotypes for study of basic virology in human and NHP derived cell lines and evaluation of pathogenesis of novel AAV serotypes in NHP and other animal models.

[0096] To achieve this goal, the genome walker system is employed to obtain 5' and 3' terminal sequences (ITRs)

and complete construction of clones containing intact novel AAV serotype genomes.

[0097] Briefly, utilizing a commercially available Universal Genome Walker Kit [Clontech], genomic DNAs from monkey tissues or cell lines that are identified as positive for the presence of AAV7 sequence are digested with Dra I, EcoR V, Pvu II and Stu I endonucleases and ligated to Genome Walker Adaptor to generate 4 individual Genome Walker Libraries (GWLs). Using DNAs from GWLs as templates, AAV7 and adjacent genomic sequences will be PCR-amplified by the adaptor primer 1 (API, provided in the kit) and an AAV7 specific primer 1, followed by a nested PCR using the adaptor primer 2 (AP2) and another AAV7 specific primer 2, both of which are internal to the first set of primers. The major PCR products from the nested PCR are cloned and characterized by sequencing analysis.

[0098] In this experiment, the primers covering the 257 bp or other signature fragment of a generic AAV genome are used for PCR amplification of cellular DNAs extracted from Human and NHP derived cell lines to identify and characterize latent AAV sequences. The identified latent AAV genomes are rescued from the positive cell lines using adenovirus helpers of different species and strains.

[0099] To isolate infectious AAV clones from NHP derived cell lines, a desired cell line is obtained from ATCC and screened by PCR to identify the 257 bp amplicon, i.e., signature region of the invention. The 257 bp PCR product is cloned and serotyped by sequencing analysis. For these cell lines containing the AAV7 sequence, the cells are infected with SV-15, a simian adenovirus purchased from ATCC, human Ad5 or transfected with plasmid construct housing the human Ad genes that are responsible for AAV helper functions. At 48 hour post infection or transfection, the cells are harvested and Hirt DNA is prepared for cloning of AAV7 genome following Xiao et al., 1999, J. Virol, 73:3994-4003.

Example 5 - Production of AAV Vectors

[0100] A pseudotyping strategy similar to that of Example 3 for AAV1/7 was employed to produce AAV2 vectors packaged with AAV1, AAV5 and AAV8 capsid proteins. Briefly, recombinant AAV genomes equipped with AAV2 ITRs were packaged by triple transfection of 293 cells with cis-plasmid, adenovirus helper plasmid and a chimeric packaging construct where the AAV2 rep gene is fused with cap genes of novel AAV serotypes. To create the chimeric packaging constructs, the Xho I site of p5E18 plasmid at 3169 bp was ablated and the modified plasmid was restricted with Xba I and Xho I in a complete digestion to remove the AAV2 cap gene and replace it with a 2267 bp Spe I/Xho I fragment containing the AAV8 cap gene [Xiao, W., et al., (1999) *J Virol* **73**, 3994-4003]. A similar cloning strategy was used for creation of chimeric packaging plasmids of AAV2/1 and AAV2/5. All recombinant vectors were purified by the standard CsCl₂ sedimentation method except for AAV2/2, which was purified by single step heparin chromatography.

[0101] Genome copy (GC) titers of AAV vectors were determined by TaqMan analysis using probes and primers targeting SV40 poly A region as described previously [Gao, G., et al., (2000) *Hum Gene Ther* **11**, 2079-91].

[0102] Vectors were constructed for each serotype for a number of *in vitro* and *in vivo* studies. Eight different transgene cassettes were incorporated into the vectors and recombinant virions were produced for each serotype. The recovery of virus, based on genome copies, is summarized in Table 4 below. The yields of vector were high for each serotype with no consistent differences between serotypes. Data presented in the table are average genome copy yields with standard deviation x 10¹³ of multiple production lots of 50 plate (150 mm) transfections.

Table 4. Production of Recombinant Vectors

	AAV2/1	AAV2/2	AAV2/5	AAV2/7	AAV2/8
CMV LacZ	7.30 ± 4.33 (n=9)	4.49 ± 2.89 (n=6)	5.19 ± 5.19 (n=8)	3.42 (n=1)	0.87 (n=1)
CMV EGFP	6.43 ± 2.42 (n=2)	3.39 ± 2.42 (n=2)	5.55 ± 6.49 (n=4)	2.98 ± 2.66 (n=2)	3.74 ± 3.88 (n=2)
TBG LacZ	4.18 (n=1)	0.23 (n=1)	0.704 ± 0.43 (n=2)	2.16 (n=1)	0.532 (n=1)
Alb A1AT	4.67 ± 0.75 (n=2)	4.77 (n=1)	4.09 (n=1)	5.04 (n=1)	2.02 (n=1)
CB A1AT	0.567 (n=1)	0.438 (n=1)	2.82 (n=1)	2.78 (n=1)	0.816 ± 0.679 (n=2)
TBG rhCG	8.51 ± 6.65 (n=6)	3.47 ± 2.09 (n=5)	5.26 ± 3.85 (n=4)	6.52 ± 3.08 (n=4)	1.83 ± 0.98 (n=5)
TBG cFIX	1.24 ± 1.29 (n=3)	0.63 ± 0.394 (n=6)	3.74 ± 2.48 (n=7)	4.05 (n=1)	15.8 ± 15.0 (n=5)

Example 6 - Serologic Analysis of Pseudotyped Vectors

[0103] C57BL/6 mice were injected with vectors of different serotypes of AAVCBA1AT vectors intramuscularly (5 x

10¹¹ GC) and serum samples were collected 34 days later. To test neutralizing and cross-neutralizing activity of sera to each serotype of AAV, sera was analyzed in a transduction based neutralizing antibody assay [Gao, G. P., et al., (1996) *J Virol* **70**, 8934-43]. More specifically, the presence of neutralizing antibodies was determined by assessing the ability of serum to inhibit transduction of 84-31 cells by reporter viruses (AAVCMVEGFP) of different serotypes. Specifically, the reporter virus AAVCMVEGFP of each serotype [at multiplicity of infection (MOI) that led to a transduction of 90% of indicator cells] was pre-incubated with heat-inactivated serum from animals that received different serotypes of AAV or from naïve mice. After 1-hour incubation at 37° C, viruses were added to 84-31 cells in 96 well plates for 48 or 72- hour, depending on the virus serotype. Expression of GFP was measured by Fluorolmagin (Molecular Dynamics) and quantified by Image Quant Software. Neutralizing antibody titers were reported as the highest serum dilution that inhibited transduction to less than 50%.

[0104] The availability of GFP expressing vectors simplified the development of an assay for neutralizing antibodies that was based on inhibition of transduction in a permissive cell line (i.e., 293 cells stably expressing E4 from Ad5). Sera to selected AAV serotypes were generated by intramuscular injection of the recombinant viruses. Neutralization of AAV transduction by 1:20 and 1:80 dilutions of the antisera was evaluated (See Table 5 below). Antisera to AAV1, AAV2, AAV5 and AAV8 neutralized transduction of the serotype to which the antiserum was generated (AAV5 and AAV8 to a lesser extent than AAV1 and AAV2) but not to the other serotype (i.e., there was no evidence of cross neutralization suggesting that AAV 8 is a truly unique serotype).

Table 5. Serological Analysis of New AAV Serotypes.

		% Infection on 84-31 cells with AAVCMVEGFP virus:									
		AAV2/1		AAV2/2		AAV2/5		AAV2/7		AAV2/8	
		Serum dilution:		Serum dilution:		Serum dilution:		Serum dilution:		Serum dilution:	
Sera:	Immunization Vector	1/20	1/80	1/20	1/80	1/20	1/80	1/20	1/80	1/20	1/80
Group 1	AAV2/1	0	0	100	100	100	100	100	100	100	100
Group 2	AAV2/2	100	100	0	0	100	100	100	100	100	100
Group 3	AAV2/5	100	100	100	100	16.5	16.5	100	100	100	100
Group 4	AAV2/7	100	100	100	100	100	100	61.5	100	100	100
Group 5	AAV2/8	100	100	100	100	100	100	100	100	26.3	60

[0105] Human sera from 52 normal subjects were screened for neutralization against selected serotypes. No serum sample was found to neutralize AAV2/7 and AAV2/8 while AAV2/2 and AAV2/1 vectors were neutralized in 20% and 10% of sera, respectively. A fraction of human pooled IgG representing a collection of 60,000 individual samples did not neutralize AAV2/7 and AAV2/8, whereas AAV2/2 and AAV2/1 vectors were neutralized at titers of serum equal to 1/1280 and 1/640, respectively.

Example 7 - In vivo Evaluation of Different Serotypes of AAV Vectors

[0106] In this study, 7 recombinant AAV genomes, AAV2CBhAIAT, AAV2AlbAIAT, AAV2CMVrhCG, AAV2TBGrhCG, AAV2TBGcFIX, AAV2CMVLacZ and AAV2TBGLacZ were packaged with capsid proteins of different serotypes. In all 7 constructs, minigene cassettes were flanked with AAV2 ITRs. cDNAs of human α -antitrypsin (AIAT) [Xiao, W., et al., (1999) *J Virol* **73**, 3994-4003] β -subunit of rhesus monkey choriogonadotropic hormone (CG) [Zoltick, P. W. & Wilson, J. M. (2000) *Mol Ther* **2**, 657-9] canine factor IX [Wang, L., et al., (1997) *Proc Natl Acad Sci USA* **94**, 11563-6] and bacterial β -galactosidase (i.e., Lac Z) genes were used as reporter genes. For liver-directed gene transfer, either mouse albumin gene promoter (Alb) [Xiao, W. (1999), cited above] or human thyroid hormone binding globulin gene promoter (TBG) [Wang (1997), cited above] was used to drive liver specific expression of reporter genes. In muscle-directed gene transfer experiments, either cytomegalovirus early promoter (CMV) or chicken β -actin promoter with CMV enhancer (CB) was employed to direct expression of reporters.

[0107] For muscle-directed gene transfer, vectors were injected into the right tibialis anterior of 4-6 week old NCR nude or C57BL/6 mice (Taconic, Germantown, NY). In liver-directed gene transfer studies, vectors were infused intraportally into 7-9 week old NCR nude or C57BL/6 mice (Taconic, Germantown, NY). Serum samples were collected intraorbitally at different time points after vector administration. Muscle and liver tissues were harvested at different time points for cryosectioning and Xgal histochemical staining from animals that received the lacZ vectors. For the re-administration experiment, C56BL/6 mice initially received AAV2/1, 2/2, 2/5, 2/7 and 2/8CBAIAT vectors intramuscularly and followed for A1AT gene expression for 7 weeks. Animals were then treated with AAV2/8TBGcFIX intraportally and studied for cFIX gene expression.

[0108] ELISA based assays were performed to quantify serum levels of hA1AT, rhCG and cFIX proteins as described previously [Gao, G. P., et al., (1996) *J Virol* **70**, 8934-43; Zoltick, P. W. & Wilson, J. M. (2000) *Mol Ther* **2**, 657-9; Wang, L., et al., *Proc Natl Acad Sci U S A* **94**, 11563-6]. The experiments were completed when animals were sacrificed for harvest of muscle and liver tissues for DNA extraction and quantitative analysis of genome copies of vectors present in target tissues by TaqMan using the same set of primers and probe as in titration of vector preparations [Zhang, Y., et al., (2001) *Mol Ther* **3**, 697-707].

[0109] The performance of vectors based on the new serotypes were evaluated in murine models of muscle and liver-directed gene transfer and compared to vectors based on the known serotypes AAV1, AAV2 and AAV5. Vectors expressing secreted proteins (alpha-antitrypsin (A1AT) and chorionic gonadotropin (CG)) were used to quantitate relative transduction efficiencies between different serotypes through ELISA analysis of sera. The cellular distribution of transduction within the target organ was evaluated using lacZ expressing vectors and X-gal histochemistry.

[0110] The performance of AAV vectors in skeletal muscle was analyzed following direct injection into the tibialis anterior muscles. Vectors contained the same AAV2 based genome with the immediate early gene of CMV or a CMV enhanced β -actin promoter driving expression of the transgene. Previous studies indicated that immune competent C57BL/6 mice elicit limited humoral responses to the human A1AT protein when expressed from AAV vectors [Xiao, W., et al., (1999) *J Virol* **73**, 3994-4003].

[0111] In each strain, AAV2/1 vector produced the highest levels of A1AT and AAV2/2 vector the lowest, with AAV2/7 and AAV2/8 vectors showing intermediate levels of expression. Peak levels of CG at 28 days following injection of nu/nu NCR mice showed the highest levels from AAV2/7 and the lowest from AAV2/2 with AAV2/8 and AAV2/1 in between. Injection of AAV2/1 and AAV2/7 lacZ vectors yielded gene expression at the injection sites in all muscle fibers with substantially fewer lacZ positive fibers observed with AAV2/2 and AAV2/8 vectors. These data indicate that the efficiency of transduction with AAV2/7 vectors in skeletal muscle is similar to that obtained with AAV2/1, which is the most efficient in skeletal muscle of the previously described serotypes [Xiao, W. (1999), cited above; Chao, H., et al., (2001) *Mol Ther* **4**, 217-22; Chao, H., et al., (2000) *Mol Ther* **2**, 619-23].

[0112] Similar murine models were used to evaluate liver-directed gene transfer. Identical doses of vector based on genome copies were infused into the portal veins of mice that were analyzed subsequently for expression of the transgene. Each vector contained an AAV2 based genome using previously described liver-specific promoters (i.e., albumin or thyroid hormone binding globulin) to drive expression of the transgene. More particularly, CMVCG and TBGCG minigene cassettes were used for muscle and liver-directed gene transfer, respectively. Levels of rhCG were defined as relative units (RUs $\times 10^3$). The data were from assaying serum samples collected at day 28, post vector administration (4 animals per group). As shown in Table 3, the impact of capsid proteins on the efficiency of transduction of A1AT vectors in nu/nu and C57BL/6 mice and CG vectors in C57BL/6 mice was consistent (See Table 6).

Table 6. Expression of β -unit of Rhesus Monkey Chorionic Gonadotropin (rhCG)

Vector	Muscle	Liver
AAV2/1	4.5 \pm 2.1	1.6 \pm 1.0
AAV2	0.5 \pm 0.1	0.7 \pm 0.3
AAV2/5	ND*	4.8 \pm 0.8
AAV2/7	14.2 \pm 2.4	8.2 \pm 4.3
AAV2/8	4.0 \pm 0.7	76.0 \pm 22.8

* Not determined in this experiment.

[0113] In all cases, AAV2/8 vectors yielded the highest levels of transgene expression that ranged from 16 to 110 greater than what was obtained with AAV2/2 vectors; expression from AAV2/5 and AAV2/7 vectors was intermediate with AAV2/7 higher than AAV2/5. Analysis of X-Gal stained liver sections of animals that received the corresponding lacZ vectors showed a correlation between the number of transduced cells and overall levels of transgene expression. DNAs extracted from livers of C57BL/6 mice who received the A1AT vectors were analyzed for abundance of vector DNA using real time PCR technology.

[0114] The amount of vector DNA found in liver 56 days after injection correlated with the levels of transgene expression (See Table 7). For this experiment, a set of probe and primers targeting the SV40 polyA region of the vector genome was used for TaqMan PCR. Values shown are means of three individual animals with standard deviations. The animals were sacrificed at day 56 to harvest liver tissues for DNA extraction. These studies indicate that AAV8 is the most efficient vector for liver-directed gene transfer due to increased numbers of transduced hepatocytes.

Table 7 - Real Time PCR Analysis for Abundance of AAV Vectors in nu/nu Mouse Liver Following Injection of 1x10¹¹ Genome Copies of Vector.

AAV vectors/Dose	Genome Copies per Cell
AAV2/1A1bA1AT	0.6 ± 0.36
AAV2A1bA1AT	0.003 ± 0.001
AAV2/5A1bA1AT	0.83 ± 0.64
AAV2/7A1bA1AT	2.2 ± 1.7
AAV2/8A1bA1AT	18 ± 11

[0115] The serologic data described above suggest that AAV2/8 vector should not be neutralized *in vivo* following immunization with the other serotypes. C57BL/6 mice received intraportal injections of AAV2/8 vector expressing canine factor IX (10¹¹ genome copies) 56 days after they received intramuscular injections of A1AT vectors of different serotypes. High levels of factor IX expression were obtained 14 days following infusion of AAV2/8 into naïve animals (17±2 µg/ml, n=4) which were not significantly different that what was observed in animals immunized with AAV2/1 (31±23 µg/ml, n=4), AAV2/2 (16 µg/ml, n=2), and AAV2/7 (12 µg/ml, n=2). This contrasts to what was observed in AAV2/8 immunized animals that were infused with the AAV2/8 factor IX vector in which no detectable factor IX was observed (< 0.1 µg/ml, n=4).

[0116] Oligonucleotides to conserved regions of the cap gene did amplify sequences from rhesus monkeys that represented unique AAVs. Identical cap signature sequences were found in multiple tissues from rhesus monkeys derived from at least two different colonies. Full-length rep and cap open reading frames were isolated and sequenced from single sources. Only the cap open reading frames of the novel AAVs were necessary to evaluate their potential as vectors because vectors with the AAV7 or AAV8 capsids were generated using the ITRs and rep from AAV2. This also simplified the comparison of different vectors since the actual vector genome is identical between different vector serotypes. In fact, the yields of recombinant vectors generated using this approach did not differ between serotypes.

[0117] Vectors based on AAV7 and AAV8 appear to be immunologically distinct (i.e., they are not neutralized by antibodies generated against other serotypes). Furthermore, sera from humans do not neutralize transduction by AAV7 and AAV8 vectors, which is a substantial advantage over the human derived AAVs currently under development for which a significant proportion of the human population has pre-existing immunity that is neutralizing [Chirmule, N., et al., (1999) *Gene Ther* 6, 1574-83].

[0118] The tropism of each new vector is favorable for *in vivo* applications. AAV2/7 vectors appear to transduce skeletal muscle as efficiently as AAV2/1, which is the serotype that confers the highest level of transduction in skeletal muscle of the primate AAVs tested to date [Xiao, W., cited above; Chou (2001), cited above, and Chou (2000), cited above]. Importantly, AAV2/8 provides a substantial advantage over the other serotypes in terms of efficiency of gene transfer to liver that until now has been relatively disappointing in terms of the numbers of hepatocytes stably transduced. AAV2/8 consistently achieved a 10 to 100-fold improvement in gene transfer efficiency as compared to the other vectors. The basis for the improved efficiency of AAV2/8 is unclear, although it presumably is due to uptake via a different receptor that is more active on the basolateral surface of hepatocytes. This improved efficiency will be quite useful in the development of liver-directed gene transfer where the number of transduced cells is critical, such as in urea cycle disorders and familial hypercholesterolemia.

[0119] Thus, the present invention provides a novel approach for isolating new AAVs based on PCR retrieval of genomic sequences. The amplified sequences were easily incorporated into vectors and tested in animals. The lack of pre-existing immunity to AAV7 and the favorable tropism of the vectors for muscle indicates that AAV7 is suitable for use as a vector in human gene therapy and other *in vivo* applications. Similarly, the lack of pre-existing immunity to the AAV serotypes of the invention, and their tropisms, renders them useful in delivery of therapeutic molecules and other useful molecules.

Example 9 - Tissue Tropism Studies

[0120] In the design of a high throughput functional screening scheme for novel AAV constructs, a non-tissue specific and highly active promoter, CB promoter (CMV enhanced chicken β actin promoter) was selected to drive an easily detectable and quantifiable reporter gene, human α anti-trypsin gene. Thus only one vector for each new AAV clone needs to be made for gene transfer studies targeting 3 different tissues, liver, lung and muscle to screen for tissue tropism of a particular AAV construct. The following table summarizes data generated from 4 novel AAV vectors in the tissue tropism studies (AAVCBA1AT), from which a novel AAV capsid clone, 44.2, was found to be a very potent gene transfer vehicle in all 3 tissues with a big lead in the lung tissue particularly. Table 8 reports data obtained (in µg A1AT/mL serum) at day 14 of the study.

EP 1 310 571 B1

Table 8

Vector	Target Tissue		
	Lung	Liver	Muscle
AAV2/1	ND	ND	45±11
AAV2/5	0.6±0.2	ND	ND
AAV2/8	ND	84±30	ND
AAV2/rh.2 (43.1)	14±7	25±7.4	35±14
AAV2/rh.10 (44.2)	23±6	53±19	46±11
AAV2/rh.13 (42.2)	3.5±2	2±0.8	3.5±1.7
AAV2/rh.21 (42.10)	3.1±2	2±1.4	4.3±2

A couple of other experiments were then performed to confirm the superior tropism of AAV 44.2 in lung tissue. First, AAV vector carried CC10hA1AT minigene for lung specific expression were pseudotyped with capsids of novel AAVs were given to Immune deficient animals (NCR nude) in equal volume (50 µl each of the original preps without dilution) via intratracheal injections as provided in the following table. In Table 9, 50 µl of each original prep per mouse, NCR Nude, detection limit ≥0.033 µg/ml, Day 28

Table 9

Vector	Total GC in 50 µl vector	µg of A1AT/ml with 50µl vector	µg of A1AT/ml with 1x10 ¹¹ vector	Relative Gene transfer as compared to rh.10 (clone 44.2)
2/1	3x10 ¹²	2.6±0.5	0.09±0.02	2.2
2/2	5.5x10 ¹¹	<0.03	<0.005	<0.1
2/5	3.6x10 ¹²	0.65±0.16	0.02±0.004	0.5
2/7	4.2x10 ¹²	1±0.53	0.02±0.01	0.5
2/8	7.5x10 ¹¹	0.9±0.7	0.12±0.09	2.9
2/ch.5 (A.3.1)	9x10 ¹²	1±0.7	0.01±0.008	0.24
2/rh.8 (43.25)	4.6x10 ¹²	26±21	0.56±0.46	13.7
2/rh.10 (44.2)	2.8x10 ¹²	115±38	4.1±1.4	100
2/rh.13 (42.2)	6x10 ¹²	7.3±0.8	0.12±0.01	2.9
2/rh.21 (42.10)	2.4x10 ¹²	9±0.9	0.38±0.04	9.3
2/rh.22 (42.11)	2.6x10 ¹²	6±0.4	0.23±0.02	5.6
2/rh.24 (42.13)	1.1x10 ¹¹	0.4±0.3	0.4±0.3	1

The vectors were also administered to immune competent animals (C57BL/6) in equal genome copies (1x10¹¹ GC) as shown in the Table 10. (1x10¹¹ GC per animal, C57BL/6, day 14, detection limit ≥0.033 µg/ml)

Table 10

AAV Vector	µg of A1AT/ml with 1x10 ¹¹ vector	Relative Gene transfer as compared to rh.10 (clone 44.2)
2/1	0.076±0.031	2.6
2/2	0.1±0.09	3.4
2/5	0.084±0.033	2.9

EP 1 310 571 B1

Table continued

AAV Vector	$\mu\text{g of A1AT/ml with } 1 \times 10^{11} \text{ vector}$	Relative Gene transfer as compared to rh.10 (clone 44.2)
2/7	0.33 ± 0.01	11
2/8	1.92 ± 1.3	2.9
2/ch.5 (A.3.1)	0.048 ± 0.004	1.6
2/rh.8 (43.25)	1.7 ± 0.7	58
2/rh.10 (44.2)	2.93 ± 1.7	100
2/rh.13 (42.2)	0.45 ± 0.15	15
2/rh.21 (42.10)	0.86 ± 0.32	29
2/rh.22 (42.11)	0.38 ± 0.18	13
2/rh.24 (42.13)	0.3 ± 0.19	10

[0121] The data from both experiments confirmed the superb tropism of clone 44.2 in lung-directed gene transfer.

[0122] Interestingly, performance of clone 44.2 in liver and muscle directed gene transfer was also outstanding, close to that of the best liver transducer, AAV8 and the best muscle transducer AAV1, suggesting that this novel AAV has some intriguing biological significance.

[0123] To study serological properties of those novel AAVs, pseudotyped AAVGFP vectors were created for immunization of rabbits and in vitro transduction of 84-31 cells in the presence and absence of antisera against different capsids. The data are summarized below:

Table 11a. Cross-NAB assay in 8431 cells and adenovirus (Adv) coinfection Infection in 8431 cells (coinfecting with Adv) with:

Serum from rabbit immunized with:	10^9 GC	10^9 GC	10^9 GC	10^{10} GC
	rh.13	rh.21	rh.22	rh.24
	AAV2/42.2	AAV2/42.10	AAV2/42.1	AAV2/42.13
AAV2/1	1/20	1/20	1/20	No NAB
AAV2/2	1/640	1/1280	1/5120	No NAB
AAV2/5	No NAB	1/40	1/160	No NAB
AAV2/7	1/81920	1/81920	1/40960	1/640
AAV2/8	1/640	1/640	1/320	1/5120
Ch.5 AAV2/A3	1/20	1/160	1/640	1/640
rh.8 AAV2/43.25	1/20	1/20	1/20	1/320
rh.10 AAV2/44.2	No NAB	No NAB	No NAB	1/5120
rh.13 AAV2/42.2	1/5120	1/5120	1/5120	No NAB
rh.21 AA V2/42.10	1/5120	1/10240	1/5120	1/20
rh.22 AAV2/42.11	1/20480	1/20480	1/40960	No NAB
rh.24 AAV2/42.13	No NAB	1/20	1/20	1/5120

EP 1 310 571 B1

Table 11b. Cross-NAB assay in 8431 cells and Adv coinfection Infection in 8431 cells (coinfecting with Adv) with:

Serum from rabbit immunized with:	10 ⁹ GC	10 ¹⁰ GC	10 ¹⁰ GC	10 ⁹ GC	10 ⁹ GC
	rh.12	ch.5	rh. 8	rh.10	rh.20
	AAV2/42.1B	AAV2/A3	AAV2/43.25	AAV2/44.2	AAV2/42.8.2
AAV2/1	No NAB	1/20480	No NAB	1/80	ND
AAV2/2	1/20	No NAB	No NAB	No NAB	ND
AAV2/5	No NAB	1/320	No NAB	No NAB	ND
AAV2/7	1/2560	1/640	1/160	1/81920	ND
AAV2/8	1/10240	1/2560	1/2560	1/81920	ND
ch.5 AAV2/A3	1/1280	1/10240	ND	1/5120	1/320
rh.8 AAV2/43.25	1/1280	ND	1/20400	1/5120	1/2560
rh.10 AAV2/44.2	1/5120	ND	ND	1/5120	1/5120
rh.13 AAV2/42.2	1/20	ND	ND	No NAB	1/320
rh.21 AAV2/42.10	1/20	ND	ND	1/40	1/80
rh.22 AAV2/42.1 1	No NAB	ND	ND	ND	No NAB
rh.24 AAV2/42.13	1/5120	ND	ND	ND	1/2560

Table 12

Titer of rabbit sera		Titer after Boosting
Vector	Titer d21	
ch.5 AAV2/A3	1/10,240	1/40,960
rh.8 AAV2/43.25	1/20,400	1/163,840
rh.10 AAV2/44.2	1/10,240	1/527,680
rh.13 AAV2/42.2	1/5,120	1/20,960
rh.21 AAV2/42.10	1/20,400	1/81,920
rh.22 AAV2/42.11	1/40,960	N D
rh.24 AAV2/42.13	1/5,120	ND

Table 13 a. Infection in 8431 cells (coinfecting with Adv) with GFP

	10 ⁹ GC/well	10 ⁹ GC/well	10 ⁹ GC/well	10 ⁹ GC/well	10 ⁹ GC/well	10 ⁹ GC/well
						ch.5
	AAV2/1	AAV2/2	AAV2/5	AAV2/7	AAV2/8	AAV2/A3
# GFU/field	128	>200	95	56	13	1
	83	>200	65	54	11	1

5
10
15
20
25
30
35
40
45
50
55

Table 13b. Infection in 8431 cells (coinfected with Adv) with GFP

	10 ⁹ GC/well	10 ⁹ GC/well	10 ⁹ GC/well	10 ⁹ GC/well	10 ⁹ GC/well	10 ⁹ GC/well	10 ⁹ GC/well
	<i>rh.8</i>	<i>rh.10</i>	<i>rh.13</i>	<i>rh.21</i>	<i>rh.22</i>	<i>rh.24</i>	<i>rh.12</i>
	AAV2/43.25	AAV2/44.2	AAV2/42.2	AAV2/42.10	AAV2/42.11	AAV2/42.13	AAV2/42.1B
# GFU/field	3	13	54	62	10	3	18
	2	12	71	60	14	2	20
			48	47	16	3	12

Example 10 - Mouse Model of Familial Hypercholesterolemia

[0124] The following experiment demonstrates that the AAV2/7 construct of the invention delivers the LDL receptor and express LDL receptor in an amount sufficient to reduce the levels of plasma cholesterol and triglycerides in animal models of familial hypercholesterolemia.

A. Vector Construction

[0125] AAV vectors packaged with AAV7 or AAV8 capsid proteins were constructed using a pseudotyping strategy [Hildinger M, *et al.*, *J. Virol* 2001; 75:6199-6203]. Recombinant AAV genomes with AAV2 inverted terminal repeats (ITR) were packaged by triple transfection of 293 cells with the *cis*-plasmid, the adenovirus helper plasmid and a chimeric packaging construct, a fusion of the capsids of the novel AAV serotypes with the rep gene of AAV2. The chimeric packaging plasmid was constructed as previously described [Hildinger et al, cited above]. The recombinant vectors were purified by the standard CsCl₂ sedimentation method. To determine the yield TaqMan (Applied Biosystems) analysis was performed using probes and primers targeting the SV40 poly(A) region of the vectors [Gao GP, *et al.*, *Hum Gene Ther.* 2000 Oct 10;11(15):2079-91]. The resulting vectors express the transgene under the control of the human thyroid hormone binding globulin gene promoter (TBG).

B. Animals

[0126] LDL receptor deficient mice on the C57Bl/6 background were purchased from the Jackson Laboratory (Bar Harbor, ME, USA) and maintained as a breeding colony. Mice were given unrestricted access to water and obtained a high fat Western Diet (high % cholesterol) starting three weeks prior vector injection. At day -7 as well at day 0, blood was obtained via retroorbital bleeds and the lipid profile evaluated. The mice were randomly divided into seven groups. The vector was injected via an intraportal injection as previously described ([Chen SJ *et al.*, *Mol Therapy* 2000; 2(3), 256-261]. Briefly, the mice were anaesthetized with ketamine and xylazine. A laparotomy was performed and the portal vein exposed. Using a 30g needle the appropriate dose of vector diluted in 100ul PBS was directly injected into the portal vein. Pressure was applied to the injection site to ensure a stop of the bleeding. The skin wound was closed and draped and the mice carefully monitored for the following day. Weekly bleeds were performed starting at day 14 after liver directed gene transfer to measure blood lipids. Two animals of each group were sacrificed at the time points week 6 and week 12 after vector injection to examine atherosclerotic plaque size as well as receptor expression. The remaining mice were sacrificed at week 20 for plaque measurement and determination of transgene expression.

Table 14

	Vector	dose	n
Group 1	AAV2/7-TBG-hLDLr	1x 10 ¹² gc	12
Group 2	AAV2/7-TBG-hLDLr	3x 10 ¹¹ gc	12
Group 3	AAV2/7-TBG-hLDLr	1x 10 ¹¹ gc	12
Group 4	AAV2/8-TBG-hLDLr	1x 10 ¹² gc	12
Group 5	AAV2/8-TBG-hLDLr	3x 10 ¹¹ gc	12
Group 6	AAV2/8-TBG-hLDLr	1x 10 ¹¹ gc	12
Group 7	AAV2/7-TBG-LacZ	1x 10 ¹¹ gc	16

C. Serum lipoprotein and liver function analysis

[0127] Blood samples were obtained from the retroorbital plexus after a 6 hour fasting period. The serum was separated from the plasma by centrifugation. The amount of plasma lipoproteins and liver transaminases in the serum were detected using an automatized clinical chemistry analyzer (ACE, Schiapparelli Biosystems, Alpha Wassermann)

D. Detection of transgene expression

[0128] LDL receptor expression was evaluated by immuno-fluorescence staining and Western blotting. For Western Blot frozen liver tissue was homogenized with lysis buffer (20 mM Tris, pH7.4, 130mM NaCl, 1% Triton X 100, proteinase inhibitor (complete, EDTA-free, Roche, Mannheim, Germany). Protein concentration was determined using the Micro

BCA Protein Assay Reagent Kit (Pierce, Rockford, IL). 40 µg of protein was resolved on 4- 15% Tris-HCl Ready Gels (Biorad, Hercules, CA) and transferred to a nitrocellulose membrane (Invitrogen,). To generate Anti-hLDL receptor antibodies a rabbit was injected intravenously with an AdhLDLr prep (1×10^{13} GC). Four weeks later the rabbit serum was obtained and used for Western Blot. A 1:100 dilution of the serum was used as a primary antibody followed by a HRP-conjugated anti-rabbit IgG and ECL chemiluminescent detection (ECL Western Blot Detection Kit, Amersham, Arlington Heights, IL).

E. Immunocytochemistry

[0129] For determination of LDL receptor expression in frozen liver sections immunohistochemistry analyses were performed. 10µm cryostat sections were either fixed in acetone for 5 minutes, or unfixed. Blocking was obtained *via* a 1 hour incubation period with 10% of goat serum. Sections were then incubated for one hour with the primary antibody at room temperature. A rabbit polyclonal antibody anti-human LDL (Biomedical Technologies Inc., Stoughton, MA) was used diluted accordingly to the instructions of the manufacturer. The sections were washed with PBS, and incubated with 1:100 diluted fluorescein goat anti-rabbit IgG (Sigma, St Louis, MO). Specimens were finally examined under fluorescence microscope Nikon Microphot-FXA. In all cases, each incubation was followed by extensive washing with PBS. Negative controls consisted of preincubation with PBS, omission of the primary antibody, and substitution of the primary antibody by an isotype-matched non-immune control antibody. The three types of controls mentioned above were performed for each experiment on the same day.

F. Gene transfer efficiency

[0130] Liver tissue was obtained after sacrificing the mice at the designated time points. The tissue was shock frozen in liquid nitrogen and stored at -80°C until further processing. DNA was extracted from the liver tissue using a QIAamp DNA Mini Kit (QIAGEN GmbH, Germany) according to the manufacturers protocol. Genome copies of AAV vectors in the liver tissue were evaluated using Taqman analysis using probes and primers against the SV40 poly(A) tail as described above.

G. Atherosclerotic plaque measurement

[0131] For the quantification of the atherosclerotic plaques in the mouse aorta the mice were anaesthetized (10% ketamine and xylazine, ip), the chest opened and the arterial system perfused with ice-cold phosphate buffered saline through the left ventricle. The aorta was then carefully harvested, slit down along the ventral midline from the aortic arch down to the femoral arteries and fixed in formalin. The lipid-rich atherosclerotic plaques were stained with Sudan IV (Sigma, Germany) and the aorta pinned out flat on a black wax surface. The image was captured with a Sony DXC-960 MD color video camera. The area of the plaque as well as of the complete aortic surface was determined using Phase 3 Imaging Systems (Media Cybernetics).

H. Clearance of I^{125} LDL

[0132] Two animals per experimental group were tested. A bolus of I^{125} -labeled LDL (generously provided by Dan Rader, U Penn) was infused slowly through the tail vein over a period of 30 sec (1,000,000 counts of [I^{125}]-LDL diluted in 100µl sterile PBS/ animal). At time points 3min, 30 min, 1.5hr, 3hr, 6hr after injection a blood sample was obtained *via* the retro-orbital plexus. The plasma was separated off from the whole blood and 10µl plasma counted in the gamma counter. Finally the fractional catabolic rate was calculated from the lipoprotein clearance data.

I. Evaluation of Liver Lipid accumulation

[0133] Oil Red Staining of frozen liver sections was performed to determine lipid accumulation. The frozen liver sections were briefly rinsed in distilled water followed by a 2 minute incubation in absolute propylene glycol. The sections were then stained in oil red solution (0.5% in propylene glycol) for 16 hours followed by counterstaining with Mayer's hematoxylin solution for 30 seconds and mounting in warmed glycerin jelly solution.

[0134] For quantification of the liver cholesterol and triglyceride content liver sections were homogenized and incubated in chloroform/methanol (2:1) overnight. After adding of 0.05% H_2SO_4 and centrifugation for 10 minutes, the lower layer of each sample was collected, divided in two aliquots and dried under nitrogen. For the cholesterol measurement the dried lipids of the first aliquot were dissolved in 1% Triton X-100 in chloroform. Once dissolved, the solution was dried under nitrogen. After dissolving the lipids in ddH_2O and incubation for 30 minutes at 37 °C the total cholesterol concentration was measured using a Total Cholesterol Kit (Wako Diagnostics). For the second aliquot the dried lipids were dissolved

in alcoholic KOH and incubated at 60°C for 30 minutes. Then 1 M MgCl₂ was added, followed by incubation on ice for 10 minutes and centrifugation at 14,000 rpm for 30 minutes. The supernatant was finally evaluated for triglycerides (Wako Diagnostics).

[0135] All of the vectors pseudotyped in an AAV2/8 or AAV2/7 capsid lowered total cholesterol, LDL and triglycerides as compared to the control. These test vectors also corrected phenotype of hypercholesterolemia in a dose-dependent manner. A reduction in plaque area for the AAV2/8 and AAV2/7 mice was observed in treated mice at the first test (2 months), and the effect was observed to persist over the length of the experiment (6 months).

Example 10 - Functional Factor IX Expression and Correction of Hemophilia

A. Knock-Out Mice

[0136] Functional canine factor IX (FIX) expression was assessed in hemophilia B mice. Vectors with capsids of AAV1, AAV2, AAV5, AAV7 or AAV8 were constructed to deliver AAV2 5' ITR - liver-specific promoter [LSP] - canine FIX - woodchuck hepatitis post-regulatory element (WPRE) - AAV2 3' ITR. The vectors were constructed as described in Wang et al, 2000, *Molecular Therapy* 2: 154-158), using the appropriate capsids.

[0137] Knock-out mice were generated as described in Wang et al, 1997, *Proc. Natl. Acad. Sci. USA* 94: 11563-11566. This model closely mimics the phenotypes of hemophilia B in human.

[0138] Vectors of different serotypes (AAV1, AAV2, AAV5, AAV7 and AAV8) were delivered as a single intraportal injection into the liver of adult hemophiliac C57Bl/6 mice in a dose of 1×10^{11} GC/mouse for the five different serotypes and one group received an AAV8 vector at a lower dose, 1×10^{10} GC/mouse. Control group was injected with 1×10^{11} GC of AAV2/8 TBG LacZ3. Each group contains 5-10 male and female mice. Mice were bled bi-weekly after vector administration.

1. ELISA

[0139] The canine FIX concentration in the mouse plasma was determined by an ELISA assay specific for canine factor IX, performed essentially as described by Axelrod et al, 1990, *Proc. Natl. Acad. Sci. USA*, 87:5173-5177 with modifications. Sheep anti-canine factor IX (Enzyme Research Laboratories) was used as primary antibody and rabbit anti-canine factor IX ((Enzyme Research Laboratories) was used as secondary antibody. Beginning at two weeks following injection, increased plasma levels of cFIX were detected for all test vectors. The increased levels were sustained at therapeutic levels throughout the length of the experiment, i.e., to 12 weeks. Therapeutic levels are considered to be 5% of normal levels, i.e., at about 250 ng/mL.

[0140] The highest levels of expression were observed for the AAV2/8 (at 10^{11}) and AAV2/7 constructs, with sustained superphysiology levels cFIX levels (ten-fold higher than the normal level). Expression levels for AAV2/8 (10^{11}) were approximately 10 fold higher than those observed for AAV2/2 and AAV2/8 (10^{10}). The lowest expression levels, although still above the therapeutic range, were observed for AAV2/5.

2. In Vitro Activated Partial Thromboplastin time (aPTT) Assay

[0141] Functional factor IX activity in plasma of the FIX knock-out mice was determined by an *in vitro* activated partial thromboplastin time (aPTT) assay-Mouse blood samples were collected from the retro-orbital plexus into 1/10 volume of citrate buffer. The aPTT assay was performed as described by Wang et al, 1997, *Proc. Natl. Acad. Sci. USA* 94: 11563-11566.

[0142] Clotting times by aPTT on plasma samples of all vector injected mice were within the normal range (approximately 60 sec) when measured at two weeks post-injection, and sustained clotting times in the normal or shorter than normal range throughout the study period (12 weeks).

[0143] Lowest sustained clotting times were observed in the animals receiving AAV2/8 (10^{11}) and AAV2/7. By week 12, AAV2/2 also induced clotting times similar to those for AAV2/8 and AAV2/7. However, this lowered clotting time was not observed for AAV2/2 until week 12, whereas lowered clotting times (in the 25 - 40 sec range) were observed for AAV2/8 and AAV2/7 beginning at week two.

[0144] Immuno-histochemistry staining on the liver tissues harvested from some of the treated mice is currently being performed. About 70-80% of hepatocytes are stained positive for canine FIX in the mouse injected with AAV2/8.cFIX vector.

B. Hemophilia B Dogs

[0145] Dogs that have a point mutation in the catalytic domain of the F.IX gene, which, based on modeling studies,

appears to render the protein unstable, suffer from hemophilia B [Evans et al, 1989, Proc. Natl. Acad. Sci. USA, 86:10095-10099]. A colony of such dogs has been maintained for more than two decades at the University of North Carolina, Chapel Hill. The homeostatic parameters of these dogs are well described and include the absence of plasma F.IX antigen, whole blood clotting times in excess of 60 minutes, whereas normal dogs are 6-8 minutes, and prolonged activated partial thromboplastin time of 50-80 seconds, whereas normal dogs are 13-28 seconds. These dogs experience recurrent spontaneous hemorrhages. Typically, significant bleeding episodes are successfully managed by the single intravenous infusion of 10 ml/kg of normal canine plasma; occasionally, repeat infusions are required to control bleeding.

[0146] Four dogs are injected intraportally with AAV.cFIX according to the schedule below. A first dog receives a single injection with AAV2/2.cFIX at a dose of 3.7×10^{11} genome copies (GC)/kg. A second dog receives a first injection of AAV2/2.cFIX (2.8×10^{11} GC/kg), followed by a second injection with AAV2/7.cFIX (2.3×10^{13} GC/kg) at day 1180. A third dog receives a single injection with AAV2/2.cFIX at a dose of 4.6×10^{12} GC/kg. The fourth dog receives an injection with AAV2/2.cFIX (2.8×10^{12} GC/kg) and an injection at day 99.5 with AAV2/7.cFIX (5×10^{12} GC/kg).

[0147] The abdomen of hemophilia dogs are aseptically and surgically opened under general anesthesia and a single infusion of vector is administered into the portal vein. The animals are protected from hemorrhage in the peri-operative period by intravenous administration of normal canine plasma. The dog is sedated, intubated to induce general anesthesia, and the abdomen shaved and prepped. After the abdomen is opened, the spleen is moved into the operative field. The splenic vein is located and a suture is loosely placed proximal to a small distal incision in the vein. A needle is rapidly inserted into the vein, then the suture loosened and a 5 F cannula is threaded to an intravenous location near the portal vein threaded to an intravenous location near the portal vein bifurcation. After hemostasis is secured and the catheter balloon inflated, approximately 5.0 ml of vector diluted in PBS is infused into the portal vein over a 5 minute interval. The vector infusion is followed by a 5.0 ml infusion of saline. The balloon is then deflated, the cannula removed and venous hemostasis is secured. The spleen is then replaced, bleeding vessels are cauterized and the operative wound is closed. The animal is extubated having tolerated the surgical procedure well. Blood samples are analyzed as described. [Wang et al, 2000, *Molecular Therapy* 2: 154-158]

[0148] Results showing correction or partial correction are anticipated for AAV2/7.

SEQUENCE LISTING

[0149]

<110> The Trustees of The University of Pennsylvania

<120> A Method of Detecting and/or Identifying Adeno-Associated Virus (AAV) Sequences and Isolating Novel Sequences Identified Thereby

<130> UPN-02735ff

<150> US 60/350,607

<151> 2001-11-13

<150> US 60/341,117

<151> 2001-12-17

<150> US 60/377,066

<151> 2002-05-01

<150> US 60/386,675

<151> 2002-06-05

<160> 120

<170> PatentIn version 3.1

<210> 1

<211> 4721

<212> DNA

<213> adeno-associated virus serotype 7

EP 1 310 571 B1

<400> 1

	ttggccactc cctctatgcg cgctcgctcg ctcggtgggg cctgcggacc aaaggtccgc	60
5	agacggcaga gctctgctct gccggcccca ccgagcgagc gagcgcgcat agagggagtg	120
	gccaactcca tcactagggg taccgcgaag cgcctccac gctgccgcgt cagcgctgac	180
	gtaaatcacg tcatagggga gtggtcctgt attagctgtc acgtgagtgc ttttgcgaca	240
10	ttttgcgaca ccacgtggcc atttgaggta tatatggccg agtgagcgag caggatctcc	300
	atthttgaccg cgaaatttga acgagcagca gccatgccgg gtttctacga gatcgtgatc	360
	aaggtgccga gcgacctgga cgagcacctg ccgggcattt ctgactcgtt tgtgaactgg	420
15	gtggccgaga aggaatggga gctgcccccg gattctgaca tggatctgaa tctgatcgag	480
	caggcacccc tgaccgtggc cgagaagctg cagcgcgact tcctgggtcca atggcgccgc	540
	gtgagtaagg ccccgaggc cctgttcttt gttcagttcg agaaggcgga gagctacttc	600
20	caccttcacg ttctggtgga gaccacgggg gtcaagtcca tggtgctagg ccgcttcctg	660
	agtcagattc gggagaagct ggtccagacc atctaccgcg gggtcgagcc cacgctgccc	720
	aactggttcg cggtgaccaa gacgcgtaat ggcgccggcg gggggaacaa ggtggtggac	780
25	gagtgtctaca tccccaaacta cctcctgccc aagaccagc ccgagctgca gtgggcgtgg	840
	actaacatgg aggagtatat aagcgcggtg ttgaacctgg ccgaacgcaa acggctcgtg	900
30		
35		
40		
45		
50		
55		

EP 1 310 571 B1

	gcgcagcacc	tgaccacgt	cagccagacg	caggagcaga	acaaggagaa	tctgaacccc	960
	aattctgacg	cgcccgtgat	caggtcaaaa	acctccgcgc	gctacatgga	gctggtcggg	1020
5	tggctggtgg	accggggcat	cacctccgag	aagcagtggg	tccaggagga	ccaggcctcg	1080
	tacatctcct	tcaacgccgc	ctccaactcg	cggtcccaga	tcaaggccgc	gctggacaat	1140
	gccggcaaga	tcatggcgct	gaccaaatcc	gcgcccgaact	acctgggtggg	gccctcgctg	1200
10	cccgcggaca	ttaaaaccaa	ccgcatctac	cgcatcctgg	agctgaacgg	gtacgatcct	1260
	gcctacgccg	gctccgtett	tctcggtctg	gcccagaaaa	agttcgggaa	gcgcaacacc	1320
	atctggctgt	ttggggccgc	caccaccggc	aagaccaaca	ttgcggaagc	catcgccac	1380
15	gccgtgccct	tctacggctg	cgtcaactgg	accaatgaga	actttccctt	caacgattgc	1440
	gtcgacaaga	tggtgatctg	gtgggaggag	ggcaagatga	cggccaagggt	cgtggagtcc	1500
	gccaaaggcca	ttctcggcgg	cagcaagggtg	cgcgtyggacc	aaaagtgcga	gtcgtccgcc	1560
20	cagatcgacc	ccacccccgt	gatcgtcacc	tccaacacca	acatgtgcgc	cgtgattgac	1620
	gggaacagca	ccaccttcga	gcaccagcag	ccgttgagg	accggatgtt	caaatttgaa	1680
	ctcaccgcc	gtctggagca	cgactttggc	aagggtgacga	agcaggaagt	caaagagttc	1740
25	ttccgctggg	ccagtgatca	cgtgaccgag	gtggcgcatg	agttctacgt	cagaaagggc	1800
	ggagccagca	aaagaccgc	ccccgatgac	gcggatataa	gcgagcccaa	gcgggcctgc	1860
	ccctcagtcg	cggatccatc	gacgtcagac	gcggaaggag	ctccgggtgga	ctttgccgac	1920
30	aggtaccaaaa	acaaatgttc	tcgtcacgcg	ggcatgattc	agatgctgtt	tccttgcaaaa	1980
	acgtgcgaga	gaatgaatca	gaatttcaac	atthgttca	cacacgggggt	cagagactgt	2040
	ttagagtgtt	tccccggcgt	gtcagaatct	caaccggctg	tcagaaaaaa	gacgtatcgg	2100
35	aaactctgcg	cgattcatca	tctgctgggg	cgggcgccc	agattgcttg	ctcggcctgc	2160
	gacctggtca	acgtggacct	ggacgactgc	gtttctgagc	aataaatgac	ttaaaccagg	2220
	tatggctgcc	gatggttatc	ttccagattg	gctcgaggac	aacctctctg	agggcattcg	2280
40	cgagtgggtg	gacctgaaac	ctggagcccc	gaaacccaaa	gccaaaccagc	aaaagcagga	2340
	caacggccgg	ggtctggtgc	ttcctggcta	caagtacctc	ggacccttca	acggactcga	2400
	caaggggggag	cccgtcaacg	cggcgagcgc	agcgccctc	gagcacgaca	aggcctacga	2460
45	ccagcagctc	aaagcgggtg	acaatccgta	cctgcgggtat	aaccacgccg	acgccgagtt	2520
	tcaggagcgt	ctgcaagaag	atacgtcatt	tgggggcaac	ctcgggcgag	cagtcttcca	2580
	ggccaagaag	cgggttctcg	aacctctcgg	tctggttgag	gaaggcgcta	agacggctcc	2640
50	tgcaaagaag	agaccggtag	agccgtcacc	tcagcgttcc	cccgaactcct	ccacgggcat	2700
	cggcaagaaa	ggccagcagc	ccgccagaaa	gagactcaat	ttcggtcaga	ctggcgactc	2760
55	agagtcagtc	cccgaacctc	aacctctcgg	agaacctcca	gcagcgccct	ctagtgtggg	2820

EP 1 310 571 B1

atctggtaca gtggctgcag gcggtggcgc accaatggca gacaataacg aaggtgccga 2880
 cggagtgggt aatgcctcag gaaattggca ttgcgattcc acatggctgg gcgacagagt 2940
 5 cattaccacc agcaccgcga cctggggcct gccacctac aacaaccacc tctacaagca 3000
 aatctccagt gaaactgcag gtagtaccaa cgacaacacc tacttcggct acagcacccc 3060
 ctgggggtat tttgacttta acagattcca ctgccacttc tcaccacgtg actggcagcg 3120
 10 actcatcaac aacaactggg gattccggcc caagaagctg cggttcaagc tcttcaacat 3180
 ccaggtaag gaggtcacga cgaatgacgg cgttacgacc atcgctaata accttaccag 3240
 cacgattcag gtattctcgg actcggata ccagctgccg tacgtcctcg gctctgcgca 3300
 15 ccagggtcgc ctgcctccgt tcccggcgga cgtcttcatg attcctcagt acggctacct 3360
 gactctcaac aatggcagtc agtctgtggg acgttcctcc ttctactgcc tggagtactt 3420
 cccctctcag atgctgagaa cgggcaacaa ctttgagttc agctacagct tcgaggacgt 3480
 20 gcctttccac agcagctacg cacacagcca gagcctggac cggctgatga atcccctcat 3540
 cgaccagtac ttgtactacc tggccagaac acagagtaac ccaggaggca cagctggcaa 3600
 tcgggaactg cagttttacc agggcgggccc ttcaactatg gccgaacaag ccaagaattg 3660
 25 gttacctgga ccttgcttcc ggcaacaaag agtctccaaa acgctggatc aaaacaacaa 3720
 cagcaacttt gcttggactg gtgccaccaa atatcacctg aacggcagaa actcgttgggt 3780
 taatcccggc gtcgccatgg caactcacaa ggacgacgag gaccgctttt tcccatccag 3840
 30 cggagtcctg atttttggaa aaactggagc aactaacaaa actacattgg aaaatgtgtt 3900
 aatgacaaat gaagaagaaa ttcgtcctac taatcctgta gccacggaag aatacgggat 3960
 agtcagcagc aacttacaag cggctaatac tgcagcccag acacaagttg tcaacaacca 4020
 35 gggagcctta cctggcatgg tctggcagaa ccgggacgtg tacctgcagg gtcccactctg 4080
 ggccaagatt cctcacacgg atggcaactt tcacccgtct cctttgatgg gcggctttgg 4140
 acttaaacat ccgcctcctc agatcctgat caagaacact cccgttcccg ctaatcctcc 4200
 40 ggaggtggtt actcctgcc agtttgcttc gttcatcaca cagtacagca ccggacaagt 4260
 cagcgtggaa atcgagtggg agctgcagaa ggaaaacagc aagcgtgga acccgagat 4320
 tcagtacacc tccaactttg aaaagcagac tgggtgtggac tttgccgttg acagccaggg 4380
 45 tgtttactct gagcctcgcc ctattggcac tcgttacctc acccgtaatc tgtaattgca 4440
 tgттаатcaa taaaccggtt gattcgtttc agttgaactt tggctctcctg tgcttcttat 4500
 cttatcggtt tccatagcaa ctggttacac attaactgct tgggtgcgct tcacgataag 4560
 50 aacactgacg tcaccgcggt acccctagtg atggagtggg ccactccctc tatgcgcgct 4620
 cgctcgcctc gtggggcctg cggaccaaag gtccgcagac ggcagagctc tgctctgccg 4680
 55 gccccaccga gcgagcgagc gcgcatagag ggagtggcca a 4721

<210> 2

<211> 737

EP 1 310 571 B1

<212> PRT

<213> capsid protein of adeno-associated virus serotype 7

<400> 2

5

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

10

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

15

Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

20

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

25

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

30

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

35

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Ala Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

40

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

45

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
180 185 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Val Ala Ala Gly Gly
195 200 205

50

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
210 215 220

55

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

EP 1 310 571 B1

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 5
 Leu Tyr Lys Gln Ile Ser Ser Glu Thr Ala Gly Ser Thr Asn Asp Asn
 260 265 270
 10
 Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300
 15
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile
 305 310 315 320
 20
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
 325 330 335
 Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
 340 345 350
 25
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
 355 360 365
 30
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
 370 375 380
 Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400
 35
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser
 405 410 415
 40
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
 420 425 430
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
 435 440 445
 45
 Arg Thr Gln Ser Asn Pro Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
 450 455 460
 50
 Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
 485 490 495
 55

EP 1 310 571 B1

5 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
500 505 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
515 520 525

10 His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
530 535 540

15 Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu
545 550 555 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
565 570 575

20 Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
580 585 590

25 Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
595 600 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
610 615 620

30 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625 630 635 640

35 Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
660 665 670

40 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

45 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Phe Glu Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705 710 715 720

50 Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

55 Leu

<210> 3

EP 1 310 571 B1

<211> 623

<212> PRT

<213> rep protein of adeno-associated virus serotype 7

5 <400> 3

1	Met	Pro	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp	15
5										10							
10	Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu	
				20					25					30			
15	Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile	
			35					40					45				
20	Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu	
			50				55					60					
25	Val	Gln	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val	
					70						75					80	
30	Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Leu	His	Val	Leu	Val	Glu	
				85						90					95		
35	Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile	
				100					105					110			
40	Arg	Glu	Lys	Leu	Val	Gln	Thr	Ile	Tyr	Arg	Gly	Val	Glu	Pro	Thr	Leu	
			115					120					125				
45	Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly	
			130				135					140					
50	Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys	
					150						155					160	
55	Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Glu	Tyr	Ile	
				165					170						175		
60	Ser	Ala	Cys	Leu	Asn	Leu	Ala	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	
				180					185					190			
65	Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Leu	Asn	
			195					200					205				
70	Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr	
			210				215					220					
75	Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Arg	Gly	Ile	Thr	Ser	Glu	Lys	
					230						235					240	

EP 1 310 571 B1

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 245 250 255
 5
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 260 265 270
 10
 Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ser
 275 280 285
 Leu Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
 290 295 300
 15
 Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
 305 310 315 320
 20
 Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
 325 330 335
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
 340 345 350
 25
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
 355 360 365
 30
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
 370 375 380
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
 385 390 395 400
 35
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
 405 410 415
 40
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
 420 425 430
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
 435 440 445
 45
 Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
 450 455 460
 50
 Glu Val Lys Glu Phe Phe Arg Trp Ala Ser Asp His Val Thr Glu Val
 465 470 475 480
 Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Ser Lys Arg Pro Ala
 485 490 495

EP 1 310 571 B1

Pro Asp Asp Ala Asp Ile Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
 500 505 510
 5
 Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
 515 520 525
 10
 Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Ile Gln Met
 530 535 540
 15
 Leu Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile
 545 550 555 560
 20
 Cys Phe Thr His Gly Val Arg Asp Cys Leu Glu Cys Phe Pro Gly Val
 565 570 575
 25
 Ser Glu Ser Gln Pro Val Val Arg Lys Lys Thr Tyr Arg Lys Leu Cys
 580 585 590
 30
 Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala
 595 600 605
 35
 Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
 610 615 620

30 <210> 4
 <211> 4393
 <212> DNA
 <213> adeno-associated virus serotype 8

35 <400> 4

40

45

50

55

EP 1 310 571 B1

	cagagagggga	gtggccaact	ccatcactag	gggtagcgcg	aagcgctcc	cacgctgccg	60
	cgtcagcgct	gacgtaaatt	acgtcatagg	ggagtgggtcc	tgtattagct	gtcacgtgag	120
5	tgcttttgcg	gcatttttgcg	acaccacgtg	gccatttgag	gtatatatgg	ccgagtgagc	180
	gagcaggatc	tccattttga	ccgcgaaatt	tgaacgagca	gcagccatgc	cgggcttcta	240
	cgagatcgtg	atcaaggtgc	cgagcgacct	ggacgagcac	ctgccgggca	tttctgactc	300
10	gtttgtgaac	tgggtggccg	agaaggaatg	ggagctgcc	ccggattctg	acatggatcg	360
	gaatctgatc	gagcaggcac	ccctgacct	ggccgagaag	ctgcagcgcg	acttcctggg	420
	ccaatggcgc	cgcgtgagta	aggccccgga	ggccctcttc	tttgttcagt	tcgagaaggg	480
15	cgagagctac	tttcacctgc	acgttctggt	cgagaccacg	ggggtcaagt	ccatggtgct	540
	aggccgcttc	ctgagtcaga	ttcgggaaaa	gcttggtcca	gaccatctac	ccgcgggggc	600
	gagccccacc	ttgccaact	ggttcgcggt	gaccaaagac	gcggtaatgg	cgccggcggg	660
20	ggggaacaag	gtggtggacg	agtgtacat	ccccaaactac	ctcctgcca	agactcagcc	720
	cgagctgcag	tgggcgtgga	ctaacatgga	ggagtatata	agcgctgct	tgaacctggc	780
25							
30							
35							
40							
45							
50							
55							

EP 1 310 571 B1

	cgagcgcaaa	cggctcgtgg	cgcagcacct	gacccacgtc	agccagacgc	aggagcagaa	840
5	caaggagaat	ctgaacccca	attctgacgc	gcccgtgatc	aggtcaaaaa	cctccgcgcg	900
	ctatatggag	ctggtcgggt	ggctgggtgga	ccggggcatc	acctccgaga	agcagtggat	960
	ccaggaggac	caggcctcgt	acatctcctt	caacgccgcc	tccaactcgc	ggtcccagat	1020
10	caaggccgcg	ctggacaatg	ccggcaagat	catggcgctg	accaaaccg	cgcccgacta	1080
	cctggtgggg	ccctcgctgc	ccgcggacat	taccagaac	cgcactacc	gcactctcgc	1140
	tctcaacggc	tacgacctg	cctacgccg	ctcgtcttt	ctcggctggg	ctcagaaaaa	1200
15	gttcgggaaa	cgcaacacca	tctggctgtt	tggaccgcc	accaccggca	agaccaacat	1260
	tgcggaagcc	atcgccacg	ccgtgccctt	ctacggctgc	gtcaactgga	ccaatgagaa	1320
	ctttcccttc	aatgattgcg	tcgacaagat	ggtgatctgg	tgggaggagg	gcaagatgac	1380
20	ggccaaggtc	gtggagtccg	ccaaggccat	tctcggcggc	agcaagggtg	gcgtggacca	1440
	aaagtgcgaag	tcgtccgccc	agatcgaccc	cacccccgtg	atcgtcacct	ccaacaccaa	1500
	catgtgcgcc	gtgattgacg	ggaacagcac	caccttcgag	caccagcagc	ctctccagga	1560
25	ccggatgttt	aagtctgaac	tcacccgccg	tctggagcac	gactttggca	aggtagacaaa	1620
	gcaggaagtc	aaagagttct	tccgctgggc	cagtgatcac	gtgaccgagg	tggcgcatga	1680
	gttttacgtc	agaaagggcg	gagccagcaa	aagaccgcc	cccgatgacg	cggataaaaag	1740
30	cgagcccaag	cgggcctgcc	cctcagtcgc	ggatccatcg	acgtcagacg	cgggaaggagc	1800
	tccgggtggac	tttgccgaca	ggtaccaaaa	caaagtgtct	cgtcacgcgg	gcattgcttca	1860
	gatgctgttt	ccctgcaaaa	cgtgcgagag	aatgaatcag	aatttcaaca	tttgcttcac	1920
35	acacggggtc	agagactgct	cagagtgttt	ccccggcgtg	tcagaatctc	aaccggctcgt	1980
	cagaaagagg	acgtatcgga	aactctgtgc	gattcatcat	ctgctggggc	gggctcccgga	2040
	gattgcttgc	tcggcctgcg	atctggtcaa	cgtggacctg	gatgactgtg	tttctgagca	2100
40	ataaatgact	taaaccaggt	atggctgccg	atggttatct	tccagattgg	ctcaggagaca	2160
	acctctctga	gggcattcgc	gagtgggtgg	cgtgaaacc	tggagccccg	aagcccaaaag	2220
	ccaaccagca	aaagcaggac	gacggccggg	gtctggtgct	tcctggctac	aagtacctcg	2280
45	gacccttcaa	cggactcgac	aagggggagc	ccgtcaacgc	ggcggacgca	gcggccctcg	2340
	agcacgacaa	ggcctacgac	cagcagctgc	aggcgggtga	caatccgtac	ctgcggtata	2400
	accacgccga	cgcgagttt	caggagcgtc	tgcaagaaga	tacgtctttt	gggggcaacc	2460
50	tcgggcgagc	agtcttccag	gccaagaagc	gggttctcga	acctctcggg	ctggttgagg	2520
	aaggcgctaa	gacggctcct	ggaaagaaga	gaccggtaga	gccatcacc	cagcgttctc	2580
	cagactcctc	tacgggcatc	ggcaagaaag	gccaacagcc	cgcagaaaa	agactcaatt	2640
55	ttggtcagac	tygcgactca	gagtcagttc	cagaccctca	acctctcgga	gaacctccag	2700

EP 1 310 571 B1

	cagcgccctc	tggtgtggga	cctaatacaa	tggtgcagc	cggtggcgca	ccaatggcag	2760
	acaataacga	aggcgccgac	ggagtgggta	gttcctcggg	aaattggcat	tgcgattcca	2820
5	catggctggg	cgacagagtc	atcaccacca	gcacccgaac	ctgggccctg	cccacctaca	2880
	acaaccacct	ctacaagcaa	atctccaacg	ggacatcggg	aggagccacc	aacgacaaca	2940
	cctacttcgg	ctacagcacc	ccctgggggt	atcttgactt	taacagattc	cactgccact	3000
10	tttcaccacg	tgactggcag	cgactcatca	acaacaactg	gggattccgg	cccaagagac	3060
	tcagcttcaa	gctcttcaac	atccagggtc	aggaggtcac	gcagaatgaa	ggcaccaaga	3120
	ccatcgccaa	taacctcacc	agcaccatcc	agggtgtttac	ggactcggag	taccagctgc	3180
15	cgtagcttct	cggtcttgcc	caccagggtc	gcctgcctcc	gttcccggcg	gacgtgttca	3240
	tgattcccca	gtacggctac	ctaactctca	acaacggtag	tcaggccgtg	ggacgctcct	3300
	ccttctactg	cctggaatac	tttccttcgc	agatgctgag	aaccggcaac	aacttccagt	3360
20	ttacttacac	cttcgaggac	gtgcctttcc	acagcagcta	cgcccacagc	cagagcttgg	3420
	accggctgat	gaatcctctg	attgaccagt	acctgtacta	cttgtctcgg	actcaaacaa	3480
	caggaggcac	ggcaaatacg	cagactcttg	gcttcagcca	aggtagggcct	aatacaatgg	3540
25	ccaatcaggc	aaagaactgg	ctgccaggac	cctgttaccg	ccaacaacgc	gtctcaacga	3600
	caaccgggca	aaacaacaat	agcaactttg	cctggactgc	tgggaccaaa	taccatctga	3660
	atggaagaaa	ttcattggct	aatcctggca	tcgctatggc	aacacacaaa	gacgacgagg	3720
30	agcgtttttt	tcccagtaac	gggatcctga	tttttggaac	acaaaatgct	gccagagaca	3780
	atgcggatta	cagcgatgtc	atgctcacca	gcgaggaaga	aatcaaaacc	actaaccttg	3840
	tggctacaga	ggaatacggg	atcgtggcag	ataacttgca	gcagcaaaac	acggctcctc	3900
35	aaattggaac	tgtcaacagc	cagggggcct	tacccggtat	ggctctggcag	aaccgggacg	3960
	tgtacctgca	gggtcccatc	tgggccaaaga	ttcctcacac	ggacggcaac	ttccaccctg	4020
40	ctccgctgat	gggggggctt	ggcctgaaac	atcctccgcc	tcagatcctg	atcaagaaca	4080
	cgctgtacc	tgcggatcct	cggaccacct	tcaaccagtc	aaagctgaac	tctttcatca	4140
	cgcaatacag	caccggacag	gtcagcgtgg	aaattgaatg	ggagctgcag	aaggaaaaca	4200
45	gcaagcgctg	gaaccccgag	atccagtaca	cctccaacta	ctacaaatct	acaagtgtgg	4260
	actttgctgt	taatacagaa	ggcgtgtact	ctgaaccccg	ccccattggc	acccgttacc	4320
	tcaccgtaa	tctgtaattg	cctgttaatc	aataaaccgg	ttgattcggt	tcagttgaac	4380
50	tttggctctc	gcg					4393

<210> 5

<211> 4385

<212> DNA

55 <213> adeno-associated virus serotype 9

<400> 5

EP 1 310 571 B1

	cagagagggga gtggccaact ccatcactag gggtaatcgc gaagcgcctc ccacgctgcc	60
	gcgtcagcgc tgacgtagat tacgtcatag gggagtggtc ctgtattagc tgtcacgtga	120
5	gtgctttttgc gacatttttg gacaccacat ggccatttga ggtatatatg gccgagttag	180
	cgagcaggat ctccattttg accgcgaaat ttgaacgagc agcagccatg ccgggcttct	240
	acgagattgt gatcaagggt ccgagcgacc tggacgagca cctgccgggc atttctgact	300
10	cttttgtgaa ctgggtggcc gagaaggaat gggagctgcc cccggattct gacatggatc	360
	ggaatctgat cgagcaggca cccctgaccg tggccgagaa gctgcagcgc gacttcctgg	420
	tccaatggcg ccgcgtgagt aaggcccgagg aggcctctct ctttgttcag ttcgagaagg	480
15	gcgagagcta ctttcacctg cacgttctgg tcgagaccac ggggggtcaag tccatggtgc	540
	taggccgctt cctgagtcag attcgggaga agctgggtcca gaccatctac cgcgggatcg	600
	agccgaccct gcccaactgg ttgcgggtga ccaagacgcg taatggcgcc ggcgggggga	660
20	acaagggtggg ggacgagtgac tacatcccca actacctct gcccaagact cagcccgagc	720
	tgcagtgggc gtggactaac atggaggagt atataagcgc gtgcttgaac ctggccgagc	780
	gcaaacggct cgtggcgag cacctgacct acgtcagcca gacgcaggag cagaacaagg	840
25	agaatctgaa cccaattct gacgcgccc tgatcaggtc aaaaacctcc gcgcgctaca	900
	tggagctggg cgggtggctg gtggaccggg gcattcacctc cgagaagcag tggatccagg	960
	aggaccaggc ctcgtagatc tcttcaacg ccgcctccaa ctgcgggtcc cagatcaagg	1020
30	ccgcgctgga caatgccggc aagatcatgg cgctgaccaa atccgcgccc gactacctgg	1080
	taggcccttc acttcgggtg gacattacgc agaaccgcat ctaccgcatc ctgcagctca	1140
	acggctacga ccctgcctac gccggctccg tctttctcgg ctgggcacaa aagaagttcg	1200
35	ggaaacgcaa caccatctgg ctgtttgggc cggccaccac gggaaagacc aacatcgag	1260
	aagccattgc ccacgccgtg cccttctacg gctgcgtcaa ctggaccaat gagaactttc	1320
	ccttcaacga ttgcgtcgac aagatgggtga tctggtggga ggagggcaag atgacggcca	1380
40	aggtcgtgga gtccgccaag gccattctcg gcggcagcaa ggtgcgcgtg gaccaaagt	1440
	gcaagtcgtc cgcccagatc gacccactc ccgtgatcgt cacctccaac accaacatgt	1500
	gcgccgtgat tgacgggaac agcaccacct tcgagacca gcagcctctc caggaccgga	1560
45	tgtttaagtt cgaactcacc cgccgtctgg agcacgactt tggcaagggtg acaaagcagg	1620
	aagtcaaaga gttcttccgc tgggccagtg atcacgtgac cgagggtggcg catgagtttt	1680
	acgtcagaaa gggcgagacc agcaaaagac ccgccccga tgacgcggat aaaagcgagc	1740
50	ccaagcgggc ctgcccctca gtcgcggatc catcgacgtc agacgcggaa ggagctccgg	1800
	tggactttgc cgacaggtac caaaacaaat gttctcgtca cgcgggcatg cttcagatgc	1860
55	tgcttccctg caaaacgtgc gagagaatga atcagaattt caacatttgc ttcacacacg	1920

EP 1 310 571 B1

	gggtcagaga	ctgctcagag	tgtttccccc	gcgtgtcaga	atctcaaccg	gtcgtcagaa	1980
	agaggacgta	tcggaaactc	tgtgcgattc	atcatctgct	ggggcgggct	cccagattg	2040
5	cttgctcggc	ctgcgatctg	gtcaacgtgg	acctggatga	ctgtgtttct	gagcaataaa	2100
	tgacttaaac	caggtatggc	tgccgatgg	tatcttcag	attggctcga	ggacaacctc	2160
	tctgagggca	ttcgcgagt	gtgggcgctg	aaacctggag	ccccgaagcc	caaagccaac	2220
10	cagcaaaagc	aggacgacgg	ccggggtctg	gtgcttcctg	gctacaagta	cctcggaccc	2280
	ttcaacggac	tcgacaaggg	ggagcccgtc	aacgcggcgg	acgcagcggc	cctcgagcac	2340
	ggcaaggcct	acgaccagca	gctgcaggcg	ggtgacaatc	cgtacctgcg	gtataaccac	2400
15	gccgacgccg	agtttcagga	gcgtctgcaa	gaagatacgt	cttttggggg	caacctcggg	2460
	cgagcagtct	tccaggccaa	gaagcgggtt	ctcgaacctc	tcggtctggt	tgaggaaggc	2520
	gctaagacgg	ctcctggaaa	gaagagaccg	gtagagccat	caccccagcg	ttctccagac	2580
20	tcctctacgg	gcatcggcaa	gaaaggccaa	cagcccgcc	gaaaaagact	caattttggt	2640
	cagactggcg	actcagagtc	agttccagac	cctcaacctc	tcggagaacc	tccagcagcg	2700
	ccctctggtg	tgggacctaa	tacaatggct	gcaggcgggtg	gcgcaccaat	ggcagacaat	2760
25	aacgaaggcg	ccgacggagt	gggtaattcc	tcgggaaatt	ggcattgcga	ttccacatgg	2820
	ctgggggaca	gagtcatcac	caccagcacc	cgaacctggg	cattgcccac	ctacaacaac	2880
	cacctctaca	agcaaacttc	caatggaaca	tcgggaggaa	gcaccaacga	caacacctac	2940
30	tttggtctaca	gcacccccctg	ggggatattt	gacttcaaca	gattccactg	ccacttctca	3000
	ccacgtgact	ggcagcgact	catcaacaac	aactggggat	tccggccaaa	gagactcaac	3060
	ttcaagctgt	tcaacatcca	ggtcaaggag	gttacgacga	acgaaggcac	caagaccatc	3120
35	gccaataaacc	ttaccagcac	cgtccaggtc	tttacggact	cggagtacca	gctaccgtac	3180
	gtcctaggct	ctgcccacca	aggatgcctg	ccaccgtttc	ctgcagacgt	cttcatgggt	3240
	cctcagtacg	gctacctgac	gctcaacaat	ggaagtcaag	cgttaggacg	ttcttctttc	3300
40	tactgtctg	aatacttccc	ttctcagatg	ctgagaaccg	gcaacaactt	tcagttcagc	3360
	tacactttcg	aggacgtgcc	ttccacagc	agctacgcac	acagccagag	tctagatcga	3420
	ctgatgaacc	ccctcatcga	ccagtaccta	tactacctgg	tcagaacaca	gacaactgga	3480
45	actgggggaa	ctcaaacttt	ggcattcagc	caagcaggcc	ctagctcaat	ggccaatcag	3540
	gctagaaact	gggtacccgg	gccttgctac	cgtcagcagc	gcgtctccac	aaccaccaac	3600
	caaaataaca	acagcaactt	tgcgtggacg	ggagctgcta	aattcaagct	gaacgggaga	3660
50	gactcgctaa	tgaatcctgg	cgtggctatg	gcatcgaca	aagacgacga	ggaccgcttc	3720
	tttccatcaa	gtggcgttct	catatttggc	aagcaaggag	ccgggaacga	tggagtcgac	3780
55	tacagccagg	tgctgattac	agatgaggaa	gaaattaaag	ccaccaaccc	tgtagccaca	3840

EP 1 310 571 B1

gaggaatacgc gagcagtggt catcaacaac caggccgcta acacgcaggc gcaaactgga 3900
 cttgtgcata accagggagt tattcctggt atgggtctggc agaaccggga cgtgtacctg 3960
 5 cagggcccta tttgggctaa aatacctcac acagatggca actttcaccg gtctcctctg 4020
 atgggtggat ttggactgaa acacccacct ccacagattc taattaaaaa tacaccagtg 4080
 10 cccgcagatc ctctctttac cttcaatcaa gccaaagtga actctttcat cagcagtgac 4140
 agcacgggac aagtcagcgt ggaaatcgag tgggagctgc agaaagaaaa cagcaagcgc 4200
 tggaatccag agatccagta tacttcaaac tactacaaat ctacaaatgt ggactttgct 4260
 15 gtcaatacca aaggtgttta ctctgagcct cgtccattg gtactcgtta cctcaccgct 4320
 aatttgtaat tgctgttaa tcaataaacc ggttaattcg tttcagttga actttggtct 4380
 ctgcg 4385
 20
 <210> 6
 <211> 4718
 <212> DNA
 <213> adeno-associated virus serotype 1
 25
 <400> 6
 30 ttgccactc cctctctgcg cgctcgtcgc ctccgtgggg cctgcggacc aaaggtccgc 60
 agacggcaga gctctgctct gccggcccca ccgagcgagc gagcgcgagc agagggagtg 120
 ggcaactcca tcaactaggg taatcgcgaa gcgcctccca cgctgccgcg tcagcgctga 180
 cgtaaattac gtcactaggg agtggctctg tattagctgt cacgtgagtg cttttgcgac 240
 35 attttgcgac accacgtggc catttagggg atatatggcc gagtgagcga gcaggatctc 300
 cattttgacc gcgaaatttg aacgagcagc agccatgccg ggcttctacg agatcgtgat 360
 caaggtgccg agcgacctgg acgagcacct gccgggcatt tctgactcgt ttgtgagctg 420
 40 ggtggccgag aaggaatggg agctgcccc ggattctgac atggatctga atctgattga 480
 gcaggcacc ctagcgtgg ccgagaagct gcagcgcgac ttctggtcc aatggcgccg 540
 cgtgagtaag gccccggagg cctctctctt tggtcagttc gagaagggcg agtcctactt 600
 45 ccacctccat attctggtgg agaccacggg ggtcaaatcc atgggtgctgg gccgcttctc 660
 gagtcagatt agggacaagc tgggtgcagc catctaccgc gggatcgagc cgacctgccc 720
 caactgggtc gcggtgacca agacgcgtaa tggcgccgga ggggggaaca aggtgggtgga 780
 50 cgagtgtctac atccccaact acctcctgcc caagactcag cccgagctgc agtgggctg 840
 gactaacatg gagaggtata taagcgctg tttgaacctg gccgagcgca aacggctcgt 900
 ggcgcagcac ctgaccacg tcagccagac ccaggagcag aacaaggaga atctgaacct 960
 55 caattctgac gcgcctgtca tccgggtcaa aacctccgcg cgctacatgg agctggctcg 1020
 gtggctggtg gaccggggca tcacctccga gaagcagtg atccaggagg accaggcctc 1080

EP 1 310 571 B1

	gtacatctcc	ttcaacgccg	cttccaactc	gcgggtcccag	atcaaggccg	ctctggacaa	1140
	tgccggcaag	atcatggcgc	tgaccaaadc	cgcgcccag	tacctggtag	gccccgctcc	1200
5	gccccgagac	attaaaacca	accgcatcta	ccgcatectg	gagctgaacg	gctacgaacc	1260
	tgctacagcc	ggctccgtct	ttctcggtcg	ggcccagaaa	aggttcggga	agcgcaacac	1320
	catctggctg	tttgggcccg	ccaccacggg	caagaccaac	atcgcggaag	ccatcgccca	1380
10	cgccgtgccc	ttctacggct	gcgtcaactg	gaccaatgag	aactttccct	tcaatgattg	1440
	cgctcgacaag	atggtgatct	ggtgggagga	gggcaagatg	acggccaagg	tcgtggagtc	1500
	cgccaaggcc	attctcggcg	gcagcaaggt	gcgctgggac	caaaagtgca	agtcgtccgc	1560
15	ccagatcgac	cccacccccg	tgatcgtcac	ctccaacacc	aacatgtgcg	ccgtgattga	1620
	cgggaaacagc	accaccttcg	agcaccagca	gccgttgacg	gaccggatgt	tcaaatttga	1680
	actcaccgcg	cgtctggagc	atgacttttg	caaggtgaca	aagcaggaag	tcaaagagtt	1740
20	cttccgctgg	gcgcaggatc	acgtgaccga	ggtggcgcat	gagttctacg	tcagaaaagg	1800
	tggagccaac	aaaagacccg	ccccgatga	cgcgagataa	agcgagccca	agcgggcctg	1860
	cccctcagtc	gcggatccat	cgacgtcaga	cgcggaagga	gctccggtgg	actttgccga	1920
25	caggtagcaa	aacaaatgtt	ctcgtcacgc	gggcatgctt	cagatgctgt	ttccctgcaa	1980
	gacatgcgag	agaatgaatc	agaatttcaa	catttgcttc	acgcacggga	cgagagactg	2040
	ttcagagtgc	ttccccggcg	tgtcagaatc	tcaaccggtc	gtcagaaaaga	ggacgtatcg	2100
30	gaaactctgt	gccattcatc	atctgctggg	gcgggctccc	gagattgctt	gctcggcctg	2160
	cgatctggtc	aacgtggacc	tggatgactg	tgtttctgag	caataaatga	cttaaaccag	2220
	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	caacctctct	gagggcattc	2280
35	gcgagtggcg	ggacttgaaa	cctggagccc	cgaagcccaa	agccaaccag	caaaagcagg	2340
	acgacggccg	gggtctggcg	cttcctggct	acaagtacct	cggacccttc	aacggactcg	2400
	acaaggggga	gcccgtcaac	gcggcgagcg	cagcgccctc	cgagcacgac	aaggcctacg	2460
40	accagcagct	caaagcgggt	gacaatccgt	acctgcggta	taaccacgcc	gacgccgagt	2520
	ttcaggagcg	tctgcaagaa	gatacgtctt	ttgggggcaa	cctcgggcga	gcagtcttcc	2580
	aggccaagaa	gcgggttctc	gaacctctcg	gtctggttga	ggaaggcgct	aagacggctc	2640
45	ctggaaagaa	acgtccggta	gagcagtcgc	cacaagagcc	agactcctcc	tcggggcatcg	2700
	gcaagacagg	ccagcagccc	gctaaaaaga	gactcaattt	tggtcagact	ggcgactcag	2760
	agtcagtccc	cgatccacaa	cctctcggag	aacctccagc	aacccccgct	gctgtgggac	2820
50	ctactacaat	ggcttcaggc	ggtggcgcac	caatggcaga	caataacgaa	ggcgccgacg	2880
	gagtggttaa	tgcttcagga	aattggcatt	gcgattccac	atggctgggc	gacagagtca	2940
55	tcaccaccag	caccgcgacc	tgggccttgc	ccacctacaa	taaccacctc	tacaagcaaa	3000

EP 1 310 571 B1

	tctccagtgc ttcaacgggg gccagcaacg acaaccacta cttcgggtac agcaccctt	3060
	gggggtatatt tgatttcaac agattccact gccacttttc accacgtgac tggcagcgac	3120
5	tcatcaacaa caattgggga ttccggccca agagactcaa cttcaaactc ttcaacatcc	3180
	aagtcaagga ggtcacgacg aatgatggcg tcacaacccat cgctaataac cttaccagca	3240
10	cggttcaagt cttctcggac tcggagtacc agcttccgta cgtcctcggc tctgcgcacc	3300
	agggctgcct ccctccgttc ccggcggacg tgttcatgat tccgcaatac ggctacctga	3360
	cgctcaacaa tggcagccaa gccgtgggac gttcatcctt ttactgcctg gaatatattcc	3420
15	cttctcagat gctgagaacg ggcaacaact ttaccttcag ctacaccttt gaggaagtgc	3480
	ctttccacag cagctacgag cacagccaga gcctggaccg gctgatgaat cctctcatcg	3540
	accaatacct gtattacctg aacagaactc aaaatcagtc cggaagtgcc caaaacaagg	3600
20	acttgctgtt tagccgtggg tctccagctg gcatgtctgt tcagcccaaa aactggctac	3660
	ctggaccctg ttatcggcag cagcgcgttt ctaaaacaaa aacagacaac aacaacagca	3720
	attttacctg gactgggtgct tcaaaatata acctcaatgg gcgtgaatcc atcatcaacc	3780
25	ctggcactgc tatggcctca cacaaagacg acgaagacaa gttctttccc atgagcgggtg	3840
	tcatgatttt tggaaaagag agcgcgggag cttcaaacac tgcattggac aatgtcatga	3900
	ttacagacga agaggaaatt aaagccacta acctgtggc caccgaaaga tttgggaccg	3960
30	tggcagtcaa tttccagagc agcagcacag acctgcgac cggagatgtg catgctatgg	4020
	gagcattacc tggcatgggtg tggcaagata gagacgtgta cctgcagggt cccatttggg	4080
	ccaaaattcc tcacacagat ggacactttc acctgtctcc tcttatgggc ggctttggac	4140
35	tcaagaacct gcctcctcag atcctcatca aaaacacgcc tgttcctgag aatcctccgg	4200
	cggagttttc agctacaaag tttgcttcat tcatcaccca atactccaca ggacaagtga	4260
	gtgtggaaat tgaatgggag ctgcagaaag aaaacagcaa gcgctggaat cccgaagtgc	4320
40	agtacacatc caattatgca aaatctgcc aagttgattt tactgtggac aacaatggac	4380
	tttatactga gcctcgcccc attggcaccg gttaccttac ccgtccctg taattacgtg	4440
	ttaatcaata aaccggttga ttcgtttcag ttgaactttg gtctcctgtc cttcttatct	4500
45	tatcggttac catgggttata gcttacacat taactgcttg gttgcgcttc gcgataaaag	4560
	acttacgtca tcgggttacc cctagtgtg gagttgccca ctccctctct gcgcgctcgc	4620
	tcgctcgggtg gggcctgcgg accaaaggtc cgcagacggc agagctctgc tctgcgggcc	4680
50	ccaccgagcg agcgagcgcg cagagaggga gtgggcaa	4718

<210> 7

<211> 4675

55 <212> DNA

<213> adeno-associated virus serotype 2

<400> 7

EP 1 310 571 B1

	ttggccactc cctctctgcg cgctcgcctcg ctcactgagg ccgggcgacc aaaggtcgcc	60
	cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgag agagggagtg	120
5	gccaaactcca tcactagggg ttctctggagg ggtggagtcg tgacgtgaat tacgtcatag	180
	ggttagggag gtcctgtatt agaggtcacg tgagtgtttt gcgacatttt gcgacaccat	240
	gtggtcacgc tgggtattta agcccagtg agcacgcagg gtctccattt tgaagcggga	300
10	ggtttgaacg cgcagccgcc atgccggggt ttacgagat tgtgattaag gtccccagcg	360
	accttgacgg gcatctgccc ggcatttctg acagctttgt gaactgggtg gccgagaagg	420
	aatgggagtt gccgccagat tctgacatgg atctgaatct gattgagcag gcaccctga	480
15	ccgtggccga gaagctgcag cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc	540
	cggaggccct tttctttgtg caatttgaga agggagagag ctacttccac atgcacgtgc	600
	tcgtggaaac caccggggtg aaatccatgg ttttgggacg tttcctgagt cagattcgcg	660
20	aaaaactgat tcagagaatt taccgcggga tcgagccgac tttgccaaac tggttcgcg	720
	tcacaaagac cagaaatggc gccggaggcg ggaacaagggt ggtggatgag tgctacatcc	780
	ccaattactt gctccccaaa acccagcctg agctccagtg ggcgtggact aatatggaac	840
25	agtatttaag cgcctgtttg aatctcacgg agcgtaaacg gttggtggcg cagcatctga	900
	cgcacgtgtc gcagacgcag gagcagaaca aagagaatca gaatcccaat tctgatgcgc	960
	cggtgatcag atcaaaaact tcagccagggt acatggagct ggtcgggtgg ctcgtggaca	1020
30	aggggattac ctcggaaga cagtggatcc aggaggacca ggcctcatac atctccttca	1080
	atgcggcctc caactcgcg tcccaaatca aggtgcctt ggacaatgcg ggaaagatta	1140
	tgagcctgac taaaaccgcc ccgactacc tgggtggcca gcagcccgtg gaggacattt	1200
35	ccagcaatcg gatattataa attttggaa taaacgggta cgatccccaat tatgcggctt	1260
	ccgtctttct gggatgggccc acgaaaaagt tcggcaagag gaacaccatc tggctgtttg	1320
	ggcctgcaac taccgggaag accaacatcg cggaggccat agcccacact gtgcccttct	1380
40	acgggtgcgt aaactggacc aatgagaact ttcccttcaa cgactgtgtc gacaagatgg	1440
	tgatctggtg ggaggagggg aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc	1500
	tcggaggaag caaggtgcgc gtggaccaga aatgcaagtc ctcggccag atagaccoga	1560
45	ctcccgtgat cgtcacctcc aacaccaaca tgtgcgccgt gattgacggg aactcaacga	1620
	ccttcgaaca ccagcagccg ttgcaagacc ggatgttcaa atttgaactc acccgccgtc	1680
	tggatcatga ctttgggaag gtcaccaagc aggaagtcaa agactttttc cgggtgggcaa	1740
50	aggatcacgt ggttgagggt gagcatgaat tctacgtcaa aaaggggtgga gccaaagaaa	1800
	gacccgcccc cagtgcgcga gatataagt agcccaaacg ggtgcgcgag tcagttgcgc	1860
55	agccatcgac gtcagacgcg gaagcttcga tcaactacgc agacaggtac caaaacaaat	1920

EP 1 310 571 B1

	gttctcgtca	cgtgggcatg	aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	1980
	atcagaattc	aaatatctgc	ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	2040
5	tgtcagaatc	tcaacccggt	tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	2100
	atcatatcat	gggaaagggt	ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	2160
	tggatgactg	catctttgaa	caataaatga	tttaaatcag	gtatggctgc	cgatggttat	2220
10	cttccagatt	ggctcgagga	cactctctct	gaaggaataa	gacagtgggtg	gaagctcaaa	2280
	cctggcccac	caccaccaa	gcccgcagag	cggcataagg	acgacagcag	gggtcttgtg	2340
	cttcctgggt	acaagtacct	cggacccttc	aacggactcg	acaagggaga	gccggtcaac	2400
15	gaggcagacg	ccgcggccct	cgagcacgta	caaagcctac	gaccggcagc	tcgacagcgg	2460
	agacaacccg	tacctcaagt	acaaccacgc	cgacgcggag	tttcaggagc	gccttaaaga	2520
	agatacgtct	tttgggggca	acctcggacg	agcagtcttc	caggcgaaaa	agagggttct	2580
20	tgaacctctg	ggcctgggtg	aggaacctgt	taagacggct	ccgggaaaaa	agaggccggt	2640
	agagcactct	cctgtggagc	cagactcctc	ctcgggaacc	ggaaaggcgg	gccagcagcc	2700
	tgcaagaaaa	agattgaatt	ttggtcagac	tggagacgca	gactcagtac	ctgaccccca	2760
25	gcctctcgga	cagccaccag	cagccccctc	tggtctggga	actaatacga	tggtctacagg	2820
	cagtggcgca	ccaatggcag	acaataacga	gggcgccgac	ggagtgggta	attcctccgg	2880
	aaattggcat	tgcgattcca	catggatggg	cgacagagtc	atcaccacca	gcacccgaac	2940
30	ctgggccctg	cccacctaca	acaaccacct	ctacaaacaa	atttccagcc	aatcaggagc	3000
	ctcgaacgac	aatcactact	ttggctacag	cacccttggt	gggtattttg	acttcaacag	3060
	attccactgc	cacttttcac	cacgtgactg	gcaaagactc	atcaacaaca	actggggatt	3120
35	ccgacccaag	agactcaact	tcaagctctt	taacattcaa	gtcaaagagg	tcacgcagaa	3180
	tgacgggtacg	acgacgattg	ccaataacct	taccagcacg	gttcagggtgt	ttactgactc	3240
	ggagtaccag	ctcccgtacg	tctcggctc	ggcgcatcaa	ggatgcctcc	cgccgttccc	3300
40	agcagacgtc	ttcatgggtg	cacagtatgg	atacctcacc	ctgaacaacg	ggagtcaggc	3360
	agtaggacgc	tcttcatttt	actgcctgga	gtactttcct	tctcagatgc	tgcgtaccgg	3420
	aaacaacttt	accttcagct	acacttttga	ggacgttcct	ttccacagca	gctacgtctca	3480
45	cagccagagt	ctggaccgtc	tcatgaatcc	tctcatcgac	cagtacctgt	attacttgag	3540
	cagaacaaac	actccaagtg	gaaccaccac	gcagtcaagg	cttcagtttt	ctcaggccgg	3600
	agcgagtgc	attcgggacc	agtctaggaa	ctggcttcct	ggaccctggt	accgccagca	3660
50	gcgagtatca	aagacatctg	cggataacaa	caacagtcaa	tactcgtgga	ctggagctac	3720
	caagtaccac	ctcaatggca	gagactctct	ggtgaatccg	gccatggcaa	gccacaagga	3780
55	cgatgaagaa	aagttttttc	ctcagagcgg	ggttctcctc	tttggaagc	aaggctcaga	3840

EP 1 310 571 B1

5 gaaaacaaat gtgaacattg aaaaggtcat gattacagac gaagaggaaa tcggaacaac 3900
 caatcccgtg gctacggagc agtatggttc tgtatctacc aacctccaga gaggcaacag 3960
 5 acaagcagct accgcagatg tcaacacaca aggcgttctt ccaggcatgg tctggcagga 4020
 cagagatgtg taccttcagg ggcccatctg ggcaaagatt ccacacacgg acggacattt 4080
 tcacccctct cccctcatgg gtggattcgg acttaaacac cctcctccac agattctcat 4140
 10 caagaacacc ccggtacctg cgaatccttc gaccaccttc agtgcggcaa agtttgcttc 4200
 cttcatcaca cagtactcca cgggacacgg tcagcgtgga gatcgagtgg gagctgcaga 4260
 aggaaaacag caaacgctgg aatcccgaat ttcagtacac ttccaactac aacaagtctg 4320
 15 ttaatcgtgg acttacgtg gataactaat gcgtgtattc agagcctcgc cccattggca 4380
 ccagatacct gactcgtaat ctgtaattgc ttgttaatca ataaaccgtt taattcgttt 4440
 cagttgaact ttggtctctg cgtatttctt tcttatctag tttccatggc tacgtagata 4500
 20 agtagcatgg cgggttaatc attaaactaca aggaaccctt agtgatggag ttggccactc 4560
 cctctctgcg cgctcgctcg ctcaactgag ccgggcgacc aaaggtcgcc cgacgcccgg 4620
 gctttgcccg ggcgccctca gtgagcgagc gagcgcgag agagggagtg gccaa 4675

25

<210> 8

<211> 4726

<212> DNA

30

<213> adeno-associated virus serotype 3

<400> 8

35 ttggccactc cctctatgcg cactcgctcg ctcggtgggg cctggcgacc aaaggtcgcc 60
 agacggacgt gctttgcacg tccggcccca ccgagcgagc gagtgcgcat agagggagtg 120
 gccaaactcca tcaactagagg tatggcagtg acgtaacgag aagcgcgaga agcgagacca 180
 40 cgcctaccag ctgcgtcagc agtcagggtg cccttttgcg acagtttgcg acaccacgtg 240
 gccgctgagg gtatatattc tcgagtgagc gaaccaggag ctccattttg accgcgaaat 300
 ttgaacgagc agcagccatg ccgggggttct acgagattgt cctgaaggtc ccgagtgacc 360
 45 tggacgagcg cctgccgggc atttctaact cgtttgttaa ctgggtggcc gagaaggaat 420
 gggacgtgcc gccggattct gacatggatc cgaatctgat tgagcaggca cccctgaccg 480
 tggccgaaaa gcttcagcgc gagttcctgg tggagtggcg ccgctgagt aaggccccgg 540
 50 aggcctctt ttttgctcag ttcgaaaagg gggagacctt cttccacctg cagtgctga 600
 ttgagaccat cgggggtcaaa tccatgggtg tcggccgcta cgtgagccag attaaagaga 660
 agctggtgac ccgcatctac cgcggggctg agccgcagct tccgaactgg ttcgcggtga 720
 55 ccaaaacgag aaatggcgcc gggggcgagg acaaggtggg ggacgactgc tacatcccca 780
 actacctgct ccccaagacc cagcccagag tccagtgggc gtggactaac atggaccagt 840

EP 1 310 571 B1

	attttaagcgc	ctgtttgaat	ctcgcggagc	gtaaaccggct	ggtggcgag	catctgacgc	900
	acgtgtcgca	gacgcaggag	cagaacaaag	agaatcagaa	ccccaattct	gacgcgccgg	960
5	tcatcaggtc	aaaaacctca	gccaggatca	tggagctggt	cgggtggctg	gtggaccgcg	1020
	ggatcacgtc	agaaaagcaa	tggattcagg	aggaccaggc	ctcgtacatc	tccttcaacg	1080
10	ccgcctccaa	ctcgcggctc	cagatcaagg	ccgcgctgga	caatgcctcc	aagatcatga	1140
	gcctgacaaa	gacggctccg	gactacctgg	tgggcagcaa	cccgccggag	gacattacca	1200
	aaaatcggat	ctaccaaate	ctggagctga	acgggtacga	tccgcagtac	gcggcctccg	1260
15	tcttctctggg	ctgggcgcaa	aagaagtctg	ggaagaggaa	caccatctgg	ctctttgggc	1320
	cggccacgac	gggtaaaacc	aacatcgcg	aagccatcgc	ccacgccgtg	cccttctacg	1380
	gctgcgtaaa	ctggaccaat	gagaactttc	ccttcaacga	ttgcgtcgac	aagatggtga	1440
20	tctggtggga	ggagggcaag	atgacggcca	aggtcgtgga	gagcgccaag	gccattctgg	1500
	gcggaagcaa	ggtgcgcgtg	gaccaaaagt	gcaagtcac	ggcccagatc	gaaccactc	1560
	ccgtgatcgt	cacctccaac	accaacatgt	gcgccgtgat	tgacgggaac	agcaccacct	1620
25	tcgagcatca	gcagccgctg	caggaccgga	tgtttgaatt	tgaacttacc	cgccgtttgg	1680
	accatgactt	tgggaaggtc	accaaacagg	aagtaaagga	ctttttccgg	tgggcttccg	1740
	atcacgtgac	tgacgtggct	catgagttct	acgtcagaaa	gggtggagct	aagaaacgcc	1800
30	ccgcctccaa	tgacgcggat	gtaagcgagc	caaaacggga	gtgcacgtca	cttgcgcagc	1860
	cgacaacgtc	agacgcggaa	gcaccggcgg	actacgcgga	caggtaccaa	aacaaatggt	1920
	ctcgtcacgt	gggcatgaat	ctgatgcttt	ttccctgtaa	aacatgcgag	agaatgaatc	1980
35	aaattttccaa	tgtctgtttt	acgcatggtc	aaagagactg	tggggaatgc	ttccctggaa	2040
	tgtcagaatc	tcaaccggtt	tctgtcgtca	aaaagaagac	ttatcagaaa	ctgtgtccaa	2100
	ttcatcatat	cctgggaagg	gcacccgaga	ttgcctgttc	ggcctgcgat	ttggccaatg	2160
40	tggacttgga	tgactgtggt	tctgagcaat	aaatgactta	aaccagggtat	ggctgctgac	2220
	ggttatcttc	cagattggct	cgaggacaac	ctttctgaag	gcattcgtga	gtggtgggct	2280
	ctgaaacctg	gagtcctca	acccaaagcg	aaccaacaac	accaggacaa	ccgtcggggt	2340
45	cttgtgcttc	cgggttacaa	atacctcgga	cccggtaacg	gactcgacaa	aggagagccg	2400
	gtcaacgagg	cggacgcggc	agccctcgaa	cacgacaaag	cttacgacca	gcagctcaag	2460
	gccggtgaca	acccgtacct	caagtacaac	cacgccgacg	ccgagtttca	ggagcgtctt	2520
50	caagaagata	cgtctttttg	gggcaacctt	ggcagagcag	tcttccaggc	caaaaagagg	2580
	atccttgagc	ctcttggtct	ggttgaggaa	gcagctaaaa	cggctcctgg	aaagaagggg	2640
	gctgtagatc	agtctcctca	ggaaccggac	tcatcatctg	gtgttgga	atcgggcaaa	2700
55	cagcctgcca	gaaaaagact	aaatttcggt	cagactggag	actcagagtc	agtcccagac	2760

EP 1 310 571 B1

	cctcaacctc tcggagaacc accagcagcc cccacaagtt tgggatctaa tacaatggct	2820
5	tcaggcggtg gcgcaccaat ggcagacaat aacgagggtg ccgatggagt gggtaattcc	2880
	tcaggaaatt ggcattgcga ttcccaatgg ctgggcgaca gagtcatcac caccagcacc	2940
	agaacctggg ccctgcccac ttacaacaac catctctaca agcaaattctc cagccaatca	3000
10	ggagcttcaa acgacaacca ctactttggc tacagcacc cttgggggta ttttgacttt	3060
	aacagattcc actgccactt ctcaccacgt gactggcagc gactcattaa caacaactgg	3120
	ggattccggc ccaagaaact cagcttcaag ctcttcaaca tccaagttag aggggtcacg	3180
15	cagaacgatg gcacgacgac tattgccaat aaccttacca gcacgggttca agtggtttacg	3240
	gactcggagt atcagctccc gtacgtgctc gggtcggcgc accaaggctg tctcccgcgc	3300
	tttcagcgg acgtcttcat ggtccctcag tatggatacc tcacctgaa caacggaagt	3360
20	caagcgggtg gacgctcatc cttttactgc ctggagtact tcccttcgca gatgctaagg	3420
	actggaaata acttccaatt cagctatacc ttcgaggatg taccttttca cagcagctac	3480
	gctcacagcc agagtttgga tcgcttgatg aatcctctta ttgatcagta tctgtactac	3540
25	ctgaacagaa cgcaaggaac aacctctgga acaaccaacc aatcacggct gcttttttagc	3600
	caggctgggc ctcagtctat gtctttgcag gccagaaatt ggctacctgg gccttgctac	3660
	cggcaacaga gactttcaaa gactgctaac gacaacaaca acagtaactt tccttggaca	3720
30	gcggccagca aatatcatct caatggccgc gactcgttg tgaatccagg accagctatg	3780
	gccagtcaca aggacgatga agaaaaattt ttccctatgc acggcaatct aatatttggc	3840
	aaagaaggga caacggcaag taacgcagaa ttagataatg taatgattac ggatgaagaa	3900
35	gagattcgta ccaccaatcc tgtggcaaca gagcagtatg gaactgtggc aaataacttg	3960
	cagagctcaa atacagctcc cagcactgga actgtcaatc atcagggggc cttacctggc	4020
	atggtgtggc aagatcgtga cgtgtacctt caaggaccta tctgggcaaa gattcctcac	4080
40	acggatggac actttcatcc ttctcctctg atgggaggct ttggactgaa acatccgcct	4140
	cctcaaataca tgatcaaaaa tactccggta ccggcaaata ctccgacgac tttcagcccgc	4200
	gccaagtttg cttcatttat cactcagtac tccactggac aggtcagcgt ggaaattgag	4260
45	tgggagctac agaaagaaaa cagcaaactg tggaatccag agattcagta cacttccaac	4320
	tacaacaagt ctgttaatgt ggactttact gtagacacta atggtgttta tagtgaacct	4380
	cgcctatttg gaaccggta tctcacacga aacttgtgaa tcctgggttaa tcaataaacc	4440
50	gtttaattcg tttcagttga actttggctc ttgtgcactt ctttatcttt atcttgtttc	4500
	catggctact gcgtagataa gcagcggcct gcggcgcttg cgcttcgcgg tttaacttg	4560
	ctggttaata tttaactctc gccatacctc tagtgatgga gttggccact ccctctatgc	4620
55	gcactcgctc gctcgggtgg gcctggcgac caaaggctgc cagacggacg tgctttgcac	4680

EP 1 310 571 B1

gtccggcccc accgagcgag cgagtgcgca tagagggagt ggccaa 4726

5 <210> 9
<211> 3098
<212> DNA
<213> new AAV serotype, clone 42.2

10 <400> 9

	gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt	60
	gcgtcgacaa gatggtgatc tgggtgggagg agggcaagat gacggccaag gtcgtggagt	120
15	ccgccaaggc cattctcggc ggcagcaagg tgcgctgga ccaaaagtgc aagtcttcg	180
	cccagatcga tcccaccccc gtgatcgta cttccaacac caacatgtgc gctgtgattg	240
	acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg	300
20	aactcaccgg ccgtctggag cacgactttg gcaagggtgac aaagcaggaa gtcaaagagt	360
	tcttcgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg	420
	gtggagccaa caagagaccc gcccccgatg acgcgataa aagcgagccc aagcgggcct	480
25	gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg	540
	acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca	600
	agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact	660
30	gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc	720
	ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct	780
	gcgatctggt caacgtggac ctggatgacc gtgtttctga gcaataaatg acttaaacca	840
35	ggtatggctg ccgatgggtta tcttccagat tggctcgagg acaacctctc tgagggcatt	900
	cgcgagtggg gggacttgaa acctggagcc ccgaaacca aagccaacca gcaaaagcag	960
	gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc	1020
40	gacaagggag agccggtcaa cgaggcagac gccgcggccc tcgagcacga caaggcctac	1080
	gacaagcagc tcgagcaggg ggacaacccg tacctcaagt acaaccacgc cgacgccgag	1140
	tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggag agcagtcttc	1200
45	caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct	1260
	cctggaaaga agagacccat agaatcccc gactcctcca cgggcatcgg caagaaaggc	1320
	cagcagcccc ctaaaaagaa gctcaacttt gggcagactg gcgactcaga gtcagtcccc	1380
50	gacccccaac ctctcggaga acctcccgcc gcgccctcag gtctgggatc tgggtacaatg	1440
	gctgcaggcg gtggcgacc aatggcagac aataacgaag gcgccgacgg agtgggtaat	1500
	gcctccggaa attggcattg cgattccaca tggctgggag acagagtcac caccaccagc	1560
55	acccgcacct gggccctgcc cacctacaac aaccacctct acaagcagat atcaagtcag	1620
	agcgggggcta ccaacgacaa ccacttcttc ggctacagca ccccctgggg ctattttgac	1680

EP 1 310 571 B1

	ttcaacagat tccactgcca cttctcacca cgtgactggc agcgactcat caacaacaac	1740
5	tgggggattcc ggcccagaaa gctgCGgttc aagttgttca acatccagggt caaggagggtc	1800
	acgacgaacg acggcggttac gaccatcgct aataacctta ccagcacgat tcagggtcttc	1860
	tcggactcgg agtaccact gccgtacgtc ctCGgtctg cgcaccagggt ctgcctccct	1920
10	ccgttccttg cggacgtggt catgattcct cagtacggat atctgactct aaacaacggc	1980
	agtcagtctg tgggacgttc ctctttctac tgCctggagt actttccttc tcagatgctg	2040
	agaacgggca ataactttga attcagctac acctttgagg aagtgccttt ccacagcagc	2100
15	tatgcgcaca gccagagcct ggaccggctg atgaatcccc tcatcgacca gtacctgtac	2160
	tacctggccc ggaccagag cactacgggg tccacaagggt agctgcagtt ccatcaggct	2220
	gggcccaca ccatggccga gcaatcaaag aactggctgc cggaccctg ttatcggcag	2280
20	cagagactgt caaaaaacat agacagcaac aacaacagta actttgcctg gaccggggcc	2340
	actaaatacc atctgaatgg tagaaattca ttaaccaacc cgggCGtagc catggccacc	2400
	aacaaggacg acgaggacca gttctttccc atcaacggag tgctggtttt tggcgaaacg	2460
25	ggggctgcca acaagacaac gctggaaaac gtgctaata gaagcgagga ggagatcaaa	2520
	accaccaatc ccgtggctac agaagaatac ggtgtggtct ccagcaacct gcaatcgctc	2580
	acggccggac ccagacaca gactgtcaac agccaggggg ctctgcccgg catggtctgg	2640
30	cagaaccggg acgtgtacct gcagggtccc atctgggcca aaattcctca cacggacggc	2700
	aactttcacc cgtctccct gatggcgga tttggactca aacaccgcc tctcaaatt	2760
	ctcatcaaaa acaccccggt acctgcta cctccagagg tgtttactcc tgccaagttt	2820
35	gcctcattta tcacgcagta cagcaccggc caggtcagcg tggagatcga gtgggaactg	2880
	cagaaagaaa acagcaaacg ctggaatcca gagattcagt acacctcaaa ttatgccaa	2940
	tctaataatg tggaatttgc tgtcaacaac gaaggggttt atactgagcc tcgccccatt	3000
40	ggcaccggtt acctcaccg taacctgtaa ttgcctgtta atcaataaac cggttaattc	3060
	gtttcagttg aactttggtc tctgcgaagg gcgaattc	3098

<210> 10
 <211> 3098
 <212> DNA
 <213> new AAV serotype, clone 16.3

<400> 10

	gaattcgccc ttcgcagaga ccaaagttca actgaaacga atcaaccggt ttattgatta	60
	acaagtaatt acaggttacg ggtgaggtaa cgggtgccaa tggggcgagg ctcagtataa	120
55	acccttcgt tgttgacagc aaattccaca ttattagact tggcataatt tgagggtgtac	180
	tgaatctctg gattccagcg tttgctgttt tctttctgca gttccactc gatctccacg	240

EP 1 310 571 B1

	ctgacctggc	cggtgctgta	ctgcgtgata	aatgaggcaa	actaggcagg	agtaaacacc	300
	cctggaggat	tagcaggtac	cggggtgttt	ttgatgagaa	tttgaggagg	cggtgttttg	360
5	agtccaaatc	cgcccatcag	gggagacggg	tgaagattgc	cgtccgtgtg	aggaattttg	420
	gcccagatgg	gaccctgcag	gtacacgtcc	cggttctgcc	agaccatgcc	gggcagagcc	480
10	ccctggctgt	tgacagtctg	tgtctggggg	ccggccgtag	acgattgcag	gttgcctggag	540
	accacaccgt	attcttctgt	agccacggga	ttggtggttt	tgatctcctc	ctcgtctggtc	600
	attagcacgt	tttccagcgt	tgtcttgttg	gcagccccc	ttttgccaaa	aaccagcact	660
15	ccgttgatgg	gaaagaactg	gccctcgtcg	tccttgtttg	tggccatggc	tacgccgggg	720
	ttggttaatg	aatttctacc	attcagatgg	tatttagtgg	ccccggtcca	ggcaaagtta	780
	ctgttgttgt	tgctgtctat	gttttttgac	agtctctgct	gccgataaca	gggtccgggc	840
20	agccagttct	ttgattgctc	ggccatggtg	ttgggccccag	cctgatggaa	ctgcagctcc	900
	cttgtggacc	ccgtagtgtc	ctgggtccgg	gccaggtagt	acaggtactg	gtcgatgagg	960
	ggattcatca	gccgggtccag	gctctggctg	tgcgcatagc	tgctgtggaa	aggcacttcc	1020
25	tcaaaggtgt	agctgaattc	aaagttaattg	ccggttctca	gcatctgaga	aggaaagtac	1080
	tccaggcagt	agaaggagga	acgtcccata	gactgactgc	cgttgtttag	agtcagatat	1140
	ccgtactgag	gaatcatgaa	cacgtccgca	gggaacggag	ggaggcagcc	ctggtgcgca	1200
30	gagccgagga	cgtacggcag	ttggtactcc	gagtccgaga	agacctgaat	cgtgctggta	1260
	aggttattag	cgatggctgt	aacgccgtcg	ttcgtcgtga	cctccttgac	ctggatgttg	1320
	aacaacttga	accgcagctt	tctgggccgg	aatccccagt	tgttgttgat	gagtcgctgc	1380
35	cagtcacgtg	gtgagaagtg	gcagtggaa	ctgttgaa	caaaatagcc	ccaggggggtg	1440
	ctgtagccga	agaagtgggt	gtcgttggtg	gccccgctct	gacttgatat	ctgctttag	1500
	agggtggtgt	tgtaggtggg	cagggcccag	gtgcgggtgc	tgggtggtgat	gactctgtcg	1560
40	cccagccatg	tggaatcgca	atgccaattt	ccggaggcat	taccactcc	gtcggcgcct	1620
	tcgttattgt	ctgccattgg	tgcgccaccg	cctgcagcca	ttgtaccaga	tcccagacct	1680
	gagggcgcg	cgaggaggtc	tccgagaggt	tgggggtcgg	gcactgactc	tgagtcgcca	1740
45	gtctgcccaa	agttgagctt	cttttttagcg	ggctgctggc	ctttcttgcc	gatgcccggtg	1800
	gaggagtctg	gggattctat	gggtctcttc	tttccaggag	ccgtcttagc	gccttctca	1860
	accagaccga	gaggttcgag	aaccgccttc	ttggcctgga	agactgctcg	cccagaggttg	1920
50	ccccaaaag	acgtatcttc	ttgaagacgc	tcctgaaact	cagcgtcggc	gtggttgtag	1980
	ttgaggtacg	ggttggtccc	ctgctcgagc	tgcttgctgt	aggccttgct	gtgctcgagg	2040
	gccgcggcgt	ctgcctcgtt	gaccggctct	cccttgctga	gtccgttgaa	gggtccgagg	2100
55	tacttgtagc	caggaagcac	cagaccccg	ccgtcgtcct	gcttttgctg	gttggctttg	2160

EP 1 310 571 B1

5 ggttttcgggg ctccagggtt caagtcccac cactcgcgaa tgccctcaga gaggttgtcc 2220
 tcgagccaat ctggaagata accatcggca gccatacctg gtttaagtca tttattgctc 2280
 agaaacacag tcatccaggt ccacgttgac cagatcgcag gccgagcaag caatctcggg 2340
 agcccccccc agcagatgat gaatggcaca gagtttccga tacgtcctct ttctgacgac 2400
 10 cggttgagat tctgacacgc cggggaaaca ttctgaacag tctctggtcc cgtgcgtgaa 2460
 gcaaatgttg aaattctgat tcattctctc gcatgtcttg cagggaaaca gcatctgaag 2520
 catgcccgcg tgacgagaac atttgttttg gtacctgtcg gcaaagtcca ccggagctcc 2580
 ttccgcgtct gacgtcgatg gatccgcgac tgaggggcag gcccgcttgg gctcgttttt 2640
 15 atccgcgtca tcgggggcgg gcctcttggt ggctccaccc tttctgacgt agaactcatg 2700
 cgccacctcg gtcacgtgat cctgcgcca gcggaagaac tctttgactt cctgctttgt 2760
 caccttgcca aagtcctgct ccagacggcg ggtgagttca aatttgaaca tccgggtcttg 2820
 20 taacggctgc tgggtgctcga aggtggtgct gttcccgtca atcacggcgc acatgttggt 2880
 gttggaagtg acgatcacgg ggggtgggatc gatctgggcg gacgacttgc acttttggtc 2940
 cacgcgcacc ttgctgccgc cgagaatggc cttggcggac tccacgacct tggccgtcat 3000
 25 cttgccctcc tcccaccaga tcaccatctt gtcgacgcaa tcgttgaagg gaaagtctc 3060
 attggtccag ttgacgcagc cgtagaaagg gcgaattc 3098

30 <210> 11
 <211> 3121
 <212> DNA
 <213> new AAV serotype, clone 29.3
 35 <400> 11

40

45

50

55

EP 1 310 571 B1

	gaattcgccc ttcgcagaga ccaaagttca actgaaacga atcaaccggt ttattgatta	60
	acaagcaatt acagattacg ggtgaggtaa cgggtgccga tggggcgagg ctcaagaataa	120
5	gtgccatctg tgttaacagc aaagtccaca tttgtagatt tgtagtagtt ggaagtgtat	180
	tgaatctctg ggttccagcg tttgctgttt tctttctgca gctcccatte aatttcacg	240
	ctgacctgtc cgggtgctgta ctgcgtgatg aacgacgccg gcttagcttg actgaaggta	300
10	gttggaggat ccgcgggaac aggtgtattc ttaatcagga tctgaggagg cgggtgtttc	360
	agtccaaagc ccccatcag cggcgaggga tgaaagtttc cgtccgtgtg aggaatcttg	420
	gccagatag gacctgcag gtacacgtcc cggttctgcc agaccatgcc aggtaaggct	480
15	ccttgactgt tgacggcccc tacaatagga gcggcgtttt gctgttgacg gttatcggcc	540
	accacgccgt actgttctgt ggccactggg ttggtggttt taattttctc ctactgggt	600
	agcataacgc tgctatagtc cacgttgctt tttccagctc cctgtttccc aaacattaag	660
20	actccgctgg acggaaaaaa tcgctcttcg tcgtccttgt gggttgccat agcgacaccg	720
	ggatttacca gagagtctct gccattcaga tgatacttgg tggcaccggt ccaggcaaag	780
25		
30		
35		
40		
45		
50		
55		

EP 1 310 571 B1

	ttgctgttgt tattttgcga cagtgtcgtg gagacgcgtt gctgccggta gcagggcccg	840
5	ggtagccagt ttttggcctg agccgacatg ttattaggcc cggcctgaga aaatagcaac	900
	tgctgagttc ctgcggtacc tcccgtggac tgagtccgag acaggtagta caggtagtgg	960
	tcgatgaggg ggttcacacag ccggtccagg ctttggctgt gcgcgtagct gctgtgaaaa	1020
10	ggcacgtcct caaactggta gctgaactca aagttgttgc ccgttctcag catttgagaa	1080
	ggaaagtact ccaggcagta gaaggaggaa cggcccacgg cctgactgcc attgttcaga	1140
	gtcaggtagc cgtactgagg aatcatgaag acgtccgccc ggaacggagg caggcagccc	1200
15	tggcgcgag agccgaggac gtacgggagc tggattccg agtccgtaa gacctgaatc	1260
	gtgctggtaa ggttattggc gatgggtctt gtgccttcat tctgcgtgac ctccctgacc	1320
	tggatgttga agagcttgaa gttgagtctc ttggggccga atccccagtt gttgttgatg	1380
20	agtcgctgcc agtcacgtgg tgagaagtgg cagtggaaac tgttaaagtc aaaatacccc	1440
	caggggggtgc tgtagccgaa gtaggtgttg tcgttggtgc ttccctccga agtcccgttg	1500
	gagatttgct tgtagaggtg gttgtttag gtggggaggg cccagggttcg ggtgctggtg	1560
25	gtgatgactc tgtcgcccag ccagtgtgaa tcgcaatgcc aatttcctga ggaactacc	1620
	actccgtcgg cgccttcgtt attgtctgcc attggagcgc caccgcctgc agccattgta	1680
	ccagatccca gaccagaggg gcctgcgggg ggttctccga ttggttgagg gtcgggcaact	1740
30	gactctgagt cgccagtctg cccaaagttg agtctctttt tcgcgggctg ctggcctttc	1800
	ttgccgatgc ccgtagtga gtctggagaa cgctgggggtg atggctctac cggctctctc	1860
	tttccaggag ccgtcttagc gccttcctca accagaccga gaggttcgag aaccgccttc	1920
35	ttggcctgga agactgctcg tccgaggttg ccccaaaag acgtatcttc ttgcagacgc	1980
	tcctgaaact cggcgctcggc gtggttatac cgcaggtacg gattgtcacc cgctttgagc	2040
	tgctggtcgt aggccttgtc gtgctcgagg gccgctgcgt ccgcccgtt gacgggctcc	2100
40	cccttgtcga gtccgttgaa ggggtccagg tacttgtagc caggaagcac cagaccccg	2160
	ccgtcgtcct gcttttgctg gttggctttg ggcttcgggg ctccagggtt cagcgccac	2220
	cactcgcgaa tgccctcaga gaggttgctc tcgagccaat ctggaagata accatcgga	2280
45	gccatacctg atctaaatca tttattgttc aaagatgcag tcatccaaat ccacattgac	2340
	cagatcgag gcagtgaag cgtctggcac ctttcccatg atatgatgaa tgtagcacag	2400
	tttctgatac gcctttttga cgacagaaac ggggttagat tctgacacgg gaaagcactc	2460
50	taaacagtct ttctgtccgt gagtgaagca gatatttgaa ttctgattca ttctctcgca	2520
	ttgtctgcag ggaaacagca tcagattcat gccacgtga cgagaacatt tgttttggtg	2580
	cctgtccgag tagttgatc aagcttcgc gtctgacgtc gatggctgc caactgactc	2640
55	gcgcaccgt ttgggctcac ttatatctgc gtcactgggg gcgggtcttt tcttggtcc	2700

EP 1 310 571 B1

	accctttttg acgtagaatt catgctccac ctcaaccacg tgatcctttg cccaccggaa	2760
5	aaagtctttg acttcctgct tgggtgacctt cccaaagtca tgatccagac ggcgggtgag	2820
	ttcaaatttg aacatccggt cttgcaacgg ctgctggtgt tcgaagggtcg ttgagttccc	2880
	gtcaatcacg gcgcacatgt tgggtgttga ggtgacgatc acgggagtcg ggtctatctg	2940
10	ggccgaggac ttgcatttct ggtccacgcg caccttgctt cctccgagaa tggctttggc	3000
	cgactccacg accttggcgg tcatcttccc ctccctccac cagatcacca tcttgtcgac	3060
	acagtcgttg aagggaaagt tctcattggt ccagttgacg cagccgtaga agggcgaatt	3120
15	c	3121

	<210> 12
	<211> 3121
20	<212> DNA
	<213> new AAV serotype, clone 29.4
	<400> 12

25

30

35

40

45

50

55

EP 1 310 571 B1

	gaattcgccc ttctacggct gcgtcaactg gaccaatgag aactttccct tcaacgactg	60
	tgtcgacaag atggtgatct ggtgggagga ggggaagatg accgccaagg tcgtggagtc	120
5	ggccaaagcc attctcggag gaagcaaggt gcgcgtggac cagaaatgca agtcctcggc	180
	ccagatagac ccgactcccg tgatcgtcac ctccaacacc aacatgtgcg ccgtgattga	240
	cgggaactca acgaccttcg aacaccagca gccgttgcaa gaccggatgt tcaaatttga	300
10	actcaccgc cgtctggatc atgactttgg gaaggtcacc aagcaggaag tcaaagactt	360
	tttcgggtgg gcaaaggatc acgtggttga ggtggagcac gaattctacg tcaaaaaggg	420
	tggagccaag aaaagacccg cccccagtga cgcagatata agtgagccca aacgggtgcg	480
15	cgagtcagtt gcgcagccat cgacgtcaga cgcggaagct tcgatcaact acgcagacag	540
	gtacccaaac aaatgttctc gtcacgcggg catgaatctg atgctgtttc cctgcagaca	600
	atgcgagaga atgaatcaga attcaaatat ctgcttcact cacggacaga aagactgttt	660
20	agagtgtttt cccgtgtcag aatctcaacc cgtttctgtc gtcaaaaagg cgtatcagaa	720
	actgtgttac attcatcata tcatgggaaa ggtgccagac gcttgactg cctgcgatct	780
	ggtcgatgtg gatttggtatg actgcatctt tgaacaataa atgatttaaa tcaggtatgg	840
25	ctgccgatgg ttatcttcca gattggctcg aggacaacct ctctgagggc attcgcgagt	900
	ggtgggcgct gaaacctgga gccccgaagc ccaaagccaa ccagcaaaag caggacggcg	960
	gccggggtct ggtgcttctt ggctacaagt acctcggacc cttcaacgga ctcgacaagg	1020
30	gggagcccg tcaacgcggcg gacgcagcgg ccctcgagca cgacaaggcc tacgaccagc	1080
	agctcaaagc gggtgacaat ccgtacctgc ggtataacca cgccgacgcc gagtttcagg	1140
	agcgtctgca agaagatacg tcttttgggg gcaacctcgg gcgagcagtc ttccaggcca	1200
35		
40		
45		
50		
55		

EP 1 310 571 B1

	agaagcgggt tctcgaaacct ctcggtcttg ttgaggaagg cgctaagacg gctcctggaa	1260
	agaagagacc ggtagagcca tcacccacgc gttctccaga ctccctctac ggcacgcgca	1320
5	agaaaggcca gcagcccgcg aaaaagagac tcaactttgg gcagactggc gactcagagt	1380
	cagtgcccgca ccctcaacca atcgggagaac ccccgccagg ccctcttggt ctgggatctg	1440
	gtacaatggc tgcaggcggg ggcgctccaa tggcagacaa taacgaaggc gccgacggag	1500
10	tgggtagttc ctcaggaaat tggcattgag attccacatg gctggggcgac tgagtcacatca	1560
	ccaccagcac ccgaacctgg gccctcccca cctacaacaa ccacctctac aagcaaattct	1620
	ccaacgggac ttcgggagga agcaccaacg acaacaccta cttcggctac agcacccctt	1680
15	gggggtatatt tgactttaac agattccact gccactttct accacgtgac tggcagcgac	1740
	tcatcaacaa caactgggga ttccggccca agagactcaa cttcaagctc ttcaacatcc	1800
	aggtcaagga ggtcacgcag aatgaaggca ccaagaccat cgccaataac cttaccagca	1860
20	cgattcaggt ctttacggac tcggaatacc agtcccgtc cgtcctcggc tctgcgcacc	1920
	agggtgcct gcctccgttc ccggcgagc tcttcacgat tcctcagtag gggtagctga	1980
	ctctgaacaa tggcagtcag gccgtgggac gttcctcctt ctactgcctg gactactttc	2040
25	cttctcaaat gctgagaacg ggcaacaact ttgagttcag ctaccagttt gaggacgtgc	2100
	cttttcacag cagctacgcg cacagccaaa gcctggaccg gctgatgaac ccctcatcg	2160
	accagtacct gtactacctg tctcggactc agtccacggg aggtaccgca ggaactcagc	2220
30	agttgctatt ttctcaggcc gggcctaata acatgtcggc tcaggccaaa aactggctac	2280
	ccgggcccctg ctaccggcag taacgcgtct ccacgacact gtcgcaaaat aacaacagca	2340
	actttgtctg gaccggtgcc accaagtatc atctgaatgg cagagactct ctggtagatc	2400
35	ccggtgtcgc tatggcaacc cacaaggacg acgaagagcg attttttccg tccagcggag	2460
	tcataatgtt tgggaaacag ggagctggaa aagacaacgt ggactatagc agcgtcatgc	2520
	taaccagtga ggaagaaatt aaaaccacca acccagtggc cacagaacag tacggcgtgg	2580
40	tggccgataa cctgcaacag caaaacgccg ctccatttgt aggggccgtc aacagtcaag	2640
	gagccttacc tggcatggc tggcagaacc gggacgtgta cctgcagggt cctacctggg	2700
	ccaagattcc tcacacggac ggaaactttc atccctcgcc gctgatggga ggctttggac	2760
45	tgaaacaccc gcctcctcag atcctgatta agaatacacc tggtcccgcg gatcctccaa	2820
	ctaccttcag tcaagctaag ctggcgctcg tcatcacgca gtacagcacc ggacaggtca	2880
	gcgtggaaat tgaatgggag ctgcaggaag aaaacagcaa acgctggaac ccagagattc	2940
50	aatacacttc caactactac aaatctacaa atgtggactt tgctgttaac acagatggca	3000
	cttattctga gcctcgcccc atcggcaccg gttacctcac ccgtaattctg taattgcttg	3060
55	ttaatcaata aaccggttga ttcgtttcag ttgaactttg gtctctgcga agggcgaaatt	3120

c

3121

5

<210> 13

<211> 3121

<212> DNA

<213> new AAV serotype, clone 29.5

10

<400> 13

15

20

25

30

35

40

45

50

55

EP 1 310 571 B1

	gaattcgccc	ttcgcgagac	caaagttcaa	ctgaaacgaa	tcaaccggtt	tattgattaa	60
	caagcaatta	cagattacgg	gtgaggtaac	gggtgccgat	ggggcgaggc	tcagaataag	120
5	tgccatctgt	gttaacagca	aagtcacat	ttgtagattt	gtagtagttg	gaagtgtatt	180
	gaatctctgg	gttcacagct	ttgctgtttt	ctttctgcag	ctccattca	atttcacgc	240
	tgacctgtcc	ggtgctgtac	tgcgtgatga	acgacgccag	cttagcttga	ctgaaggtag	300
10	ttggaggatc	cgcggaaca	ggtgtattct	taatcaggat	ctgaggaggc	gggtgtttca	360
	gtccaaagcc	tcccatcagc	ggcgagggat	gaaagtttcc	gtccgtgtga	ggaatcttgg	420
	cccagatagg	accctgcagg	tacacgtccc	ggttctgcc	gaccatgcc	ggtaaggctc	480
15	cttgactgtt	gacggcccct	acaataggag	cggcgttttg	ctggtgcagg	ttatcggcca	540
	ccacgccgta	ctgttctgtg	gccactgggt	tggtggtttt	aatttcttcc	tcactggtta	600
	gcataacgct	gctatagtcc	acgttgtctt	ttccagctcc	ctgtttccca	aacattaaga	660
20	ctccgctgga	cggaaaaaat	cgctcttcgt	cgctcttggt	ggttgccata	gcgacaccgg	720
	gatttaccag	agagtctctg	ccattcagat	gatacttggt	ggcaccggtc	caggcaaagt	780
	tgctgttgtc	attttgcgac	agtgtcgtgg	agacgcgttg	ctgccggtag	cagggcccgg	840
25	gtagccagtt	tttggcctga	gccgacatgt	tattaggccc	ggcctgagaa	aatagcaact	900
	gctgagttcc	tgcggtacct	cccgtggact	gagtccgaga	caggtagtac	aggtactggt	960
	cgatgagggg	gttcatcagc	cgggtccaggc	tttggctgtg	cgcgtagctg	ctgtgaaaag	1020
30	gcacgtcctc	aaactggtag	ctgaactcaa	agttgttgcc	cgttctcagc	atttgagaag	1080
	gaaagtactc	caggcagtag	aaggaggaac	ggccacggc	ctgactgcc	ttgttcagag	1140
	tcaggtagcc	gtactgagga	atcatgaaga	cgcccgccgg	gaacggaggc	aggcagccct	1200
35	ggtgcgcaga	gccgaggacg	tacgggagct	ggtattccga	gtccgtaaag	acctgaatcg	1260
	tgctggtaag	gttattggcg	atggtcttgg	tgccttcatt	ctgcgtgacc	tccttgacct	1320
	ggatgttgaa	gagcttgaag	ttgaggctct	tggggccgga	tcccagttg	ttgttgatga	1380
40	gtcgtgcca	gtcacgtggt	gagaagtggc	agtggaatct	gttaaagtca	aaataccccc	1440
	agggggtgct	gtagccgaag	taggtgttgt	cgttggtgct	tcctcccga	gtcccgttgg	1500
	agatttgctt	gtagagggtg	ttgtttagg	tggggagggg	ccagggttcg	gtgctggtgg	1560
45	tgatgactcc	gtcgcccagc	catgtggaat	cgcaatgcc	atttcctgag	gaactacca	1620
	ctccgtcggc	gccttcgtta	ttgtctgcca	ttggagcgcc	accgcctgca	gccattgtac	1680

50

55

EP 1 310 571 B1

	cagatcccag accagagggg cctgcggggg gttctccgat tggttgaggg tcgggcaactg	1740
	actctgagtc gccagtctgc ccaaagtga gtctcttttt cgcgggctgc tggcctttct	1800
5	tgccgatgcc cgtagaggag tctggagaac gctgggggtga tggctctacc ggtctcttct	1860
	ttccaggagc cgtcttagcg ccttcctcaa ccagaccgag aggttcgaga acccgcttct	1920
	tggcctggaa gactgctcgc ccgaggttgc ccccaaaaga cgtatcttct tgcagacgct	1980
10	cctgaaactc ggcgtcggcg tggttatacc gcaggtacgg attgtcacc gctttgagct	2040
	gctggtcgtg ggccttgtcg tgctcgaggg ccgctgcgtc cgccgcgttg acgggctccc	2100
	ccttgtcgag tccgttgaag ggtccgaggt actttagacc aggaagcacc agaccccggc	2160
15	cgctcgtcctg cttttgctgg ttggctttgg gcttcggggc tccaggtttc agcgcccacc	2220
	actcgcgaat gccctcagag aggttgtcct cgagccaatc tggaaagataa ccatcggcag	2280
	ccatacctga tttaaatcat ttattgttca aagatgcagt catccaaatc cacattgacc	2340
20	agatcgcagg cagtgaagc gtctggcacc tttcccatga tatgatgaat gtagcacagt	2400
	ttctgatacg cctttttgac gacagaaacg ggttgagatt ctgacacggg aaagcactct	2460
	aaacagtctt tctgtccgtg agtgaagcag atatttgaat tctgattcat tctctcgcat	2520
25	tgtctgcagg gaaacagcat cagattcatg cccacgtgac gagaacattt gttttggtac	2580
	ctgtctgcgt agttgatcga agcttccgcg tctgacgtcg atggctgcgc aactgactcg	2640
	cgcacccggt tgggctcact tatatctgcg tcaactggggg cgggtctttt cttgggtcca	2700
30	ccctttttga cgtagaattc atgctccacc tcaaccacgt gatcctttgc ccaccggaaa	2760
	aagtctttga cttcctgctt ggtgaccttc ccaaagtcag gatccagacg gcgggtgagt	2820
	tcaaatttga acatccggtc ttgcaacggc tgctggtggt cgaaggctcg tgagttcccg	2880
35	tcaatcacgg cgcacatgtt ggtgttgag gtgacgatca cgggagtcgg gtctatctgg	2940
	gccgaggact tgcatttctg gtccacgcgc accttgcttc ctccgagaat ggctttggcc	3000
	gactccacga ccttggcggg catcttcccc tctcccacc agatcaccat cttgtcgaca	3060
40	cagtcgttga agggaaagt ctcattggtc cagttgacgc agccgtagaa agggcgaatt	3120
	c	3121
45	<210> 14 <211> 3131 <212> DNA <213> new AAV serotype, clone 1-3	
50	<400> 14	
	gcggccgcga attcgccctt ggctgcgtca actggaccaa tgagaacttt cccttcaatg	60
55	attgcgtcga caagatggtg atctggtggg aggagggcaa gatgacggcc aaggtcgtgg	120
	agtccgccaa ggccattctc ggcggcagca aggtgcgcgt ggacccaaaag tgcaagtcgt	180

EP 1 310 571 B1

	ccgcccagat	cgaccccacc	cccgtgatcg	tcacctccaa	caccaacatg	tgcgccgtga	240
	ttgacgggaa	cagcaccacc	ttcgagcacc	agcagcctct	ccaggaccgg	atgtttaagt	300
5	tcgaactcac	ccgccgtctg	gagcacgact	ttggcaaggt	gacaaagcag	gaagtcaaag	360
	agttcttccg	ctggggcagt	gatcacgtga	ccgaggtggc	gcatgagttt	tacgtcagaa	420
10	agggcggagc	cagcaaaaga	cccgcccccg	atgacgcgga	taaaagcgag	cccaagcggg	480
	cctgcccttc	agtcgcggat	ccatcgacgt	cagacgcgga	aggagctccg	gtggactttg	540
	ccgacaggta	ccaaaacaaa	tgttctctgc	acgcgggcat	gcttcagatg	ctgtttccct	600
15	gcaaaacgtg	cgagagaatg	aatcggaatt	tcaacatttg	cttcacacac	ggggtcagag	660
	actgctcaga	gtgtttcccc	ggcgtgtcag	aatctcaacc	ggtcgtcaga	aagaggacgt	720
	atcggaact	ccgtgcgatt	catcatctgc	tggggcgggc	tcccagatt	gcttgctcgg	780
20	cctgcgatct	ggtcaacgtg	gacctggatg	actgtgtttc	tgagcaataa	atgacttaaa	840
	ccaggtatgg	ctgccgatgg	ttatcttcca	gattggctcg	aggacaacct	ctctgagggc	900
	attcgcgagt	ggtgggctgt	gaaacctgga	gccccgaagc	ccaaagccaa	ccagcaaaag	960
25	caggacgacg	gccggggctt	ggtgcttcct	ggctacaagt	acctcggacc	cttcaacgga	1020
	ctcgacaagg	gggagcccg	caacgcggcg	gacgcagcgg	ccctcgagca	cgacaaggct	1080
	tacgaccagc	agctgcaggc	gggtgacaat	ccgtacctgc	ggtataacca	cgccgacgcc	1140
30	gagtttcagg	agcgtctgca	agaagatacg	tcttttgggg	gcaacctcgg	gcgagcagtc	1200
	ttccaggcca	agaagcgggt	tctcgaacct	ctcgggtctg	ttgaggaagg	cgctaagacg	1260
	gctcctggaa	agaagagacc	ggtagagcca	tcaccccagc	gttctccaga	ctcctctacg	1320
35	ggcatcggca	agaaaggcca	acagcccggc	agaaaaagac	tcaatttttg	tcagactggc	1380
	gactcagagt	cagttccaga	ccctcaacct	ctcggagaac	ctccagcagc	gccctctggt	1440
	gtgggaccta	atacaatggc	tgcaggcggg	ggcgcaccaa	tggcagacaa	taacgaaggc	1500
40	gccgacggag	tgggtagttc	ctcgggaaat	tggcattgcy	attccacatg	gctgggcyac	1560
	agagtcatca	ccaccagcac	ccgaacctgg	gccctgcccc	cctacaacaa	ccacctctac	1620
	aagcaaattct	ccaacgggac	atcgggagga	gccaccaacg	acaacaccta	cttcggctac	1680
45	agcaccctct	gggggtatct	tgactttaac	agattccact	gccacctttc	accacgtgac	1740
	tggcagcgac	tcatcaacaa	caactgggga	ttccgaccca	agagactcag	cttcaagctc	1800
	ttcaacatcc	aggtcaagga	ggtcacgcag	aatgaaggca	ccaagaccat	cgccaataac	1860
50	ctcaccagca	ccatccaggt	gtttacggac	tcggagtacc	agctgccgta	cgttctcggc	1920
	tctgtccacc	agggctgcct	gcctccgttc	ccggcggagc	tgttcatgat	tcccagctac	1980
	ggctaccta	cactcaacaa	cggtagtcag	gccgtgggac	gctcctcctt	ctactgcctg	2040
55	gaatactttc	cttcgcagat	gctgagaacc	ggcaacaact	tccagtttac	ttacaccttc	2100

EP 1 310 571 B1

	gaggacgtgc ctttccacag cagctacgcc cacagctaga gcttggaccg gctgatgaat	2160
	cctctgattg accagtacct gtactacttg tctcggactc aaacaacagg aggcacggca	2220
5	aatacgcaga ctctgggctt cagccaaggt gggcctaata caatggccaa tcaggcaaag	2280
	aactggctgc caggaccctg ttaccgcca caacgcgtct caacgacaac cgggcaaaac	2340
10	aacaatagca actttgcctg gactgctggg accaaatacc atctgaatgg aagaaattca	2400
	ttggctaatac ctggcatcgc tatggcaaca cacaagacg acgaggagcg tttttttccc	2460
	agtaacggga tcctgatttt tggcaaacaa aatgctgcca gagacaatgc ggattacagc	2520
15	gatgtcatgc tcaccagcga ggaagaaatc aaaaccacta accctgtggc tacagaggaa	2580
	tacgggtatcg tggcagataa cttgcagcag caaaacacgg ctcctcaa at tggaactgtc	2640
	aacagccagg gggccttacc cgggtatggc tggcagaacc gggacgtgta cctgcagggt	2700
20	cccatctggg ccaagattcc tcacacggac ggcaacttcc acccgtctcc gctgatgggc	2760
	ggcttttgcc tgaaacatcc tccgcctcag atcctgatca agaacacgcc tgtacctgcg	2820
	gatectccga ccaccttcaa ccagtcaaag ctgaactctt tcatcacgca atacagcacc	2880
25	ggacagggtca gcgtggaaat tgaatgggag ctgcagaagg aaaacagcaa gcgctggaac	2940
	cccagatcc agtacacctc caactactac aaatctataa gtgtggactt tgctgttaat	3000
	acagaaggcg tgtactctga accccgcccc attggcaccc gttacctcac ccgtaatctg	3060
30	taattgcctg ttaatcaata aaccggttga ttcgtttcag ttgaactttg gtctctgcga	3120
	agggcgaatt c	3131

35	<210> 15
	<211> 3127
	<212> DNA
	<213> new AAV serotype, clone 13-3b
40	<400> 15

45

50

55

EP 1 310 571 B1

	gcggccgcga attcgccctt cgcagagacc aaagttcaac tgaaacgaat caaccgggttt	60
	attgattaac atgcaattac agattacggg tgaggtaacg agtgccaata gggcgaggct	120
5	cagagtaaac accctggctg tcaacggcaa agtccacacc agtctgcttt tcaaagttgg	180
	aggtgtactg aatctccggg tcccagcgct tgctgttttc cttctgcagc tcccactcga	240
	tttccacgct gacttgctcg gtgctgtact gtgtgatgaa cgaagcaaac ttggcaggag	300
10	taaacacctc cggaggatta gcgggaacgg gagtgttctt gatcaggatc tgaggaggcg	360
	gatgtttaag tccaaagccg cccatcaaag gagacgggtg aaagttgcca tccgtgtgag	420
	gaatcttggc ccagatggga ccctgcaggt acacgtcccg gttctgccag accatgccag	480
15	gtaaggctcc ctggttggtg acaacttggtg tctgggctgc agtattagcc gcttgtaagt	540
	tgctgctgac tatcccgat tcttccgtgg ctacaggatt agtaggacga atttcttctt	600
	catttgatcat taacacattt tccaatgtag ttttgtagt tgctccagtt tttccaaaaa	660
20		
25		
30		
35		
40		
45		
50		
55		

EP 1 310 571 B1

	tcaggactcc gctggatggg aaaaagcggg cctcgtcgtc cttgtgagtt gccatggcga	720
5	cgccgggatt aaccaacgag tttctgccgt tcaggtgata tttgggtggca ccagtccaag	780
	caaagttgct gttgtttgtt tgatccagcg ttttgagagc cctttgttgc cggaagcagg	840
	gtccaggtaa ccaattcttg gcttgttcgg ccatagttga agggccgccc tggtaaaact	900
10	gcagttcccg attgccagct gtgcctcctg ggtcactctg tgttctggcc aggtagtaca	960
	agtactggtc gatgagggga ttcatacagc ggtccaggct ctggctgtgt gcgtagctgc	1020
	tgtggaaagg cacgtcctcg aagctgtagc tgaactcaaa gttgttgccc gttctcagca	1080
15	tctgagaggg gaagtactcc aggcagtaga aggaggaacg tcccacagac tgaactgcat	1140
	tgttgagagt caggtagccg tactgaggaa tcatgaagac gtccgcccgg aacggaggca	1200
	ggcagccctg gtgcgcagag ccgaggacgt acggcagctg gtattccgag tccgagaata	1260
20	cctgaatcgt gctggtaagg ttattagcga tggtcgtaac gccgtcattc gtcgtgacct	1320
	ccttgacctg gatgttgaag agcttgaacc gcagcttctt gggccggaat cccagttgt	1380
	tgttgatgag tcgctgccag tcacgtggtg agaagtggca gtggaatctg ttaaagtcaa	1440
25	aataccccca gggggtgctg tagccgaagt aggtgttgtc gttggtacta cctgcagttt	1500
	cactggagat ttgctcgtag aggtggttgt ttaggtggg cagggcccag gttcgggtgc	1560
	tgggtgtaat gactctgtcg ccagccatg tggaatcgca atgccaattt cctgaggcat	1620
30	taccactcc gtcggcacct tcgttattgt ctgccattgg tgcgccaccg cctgcagcca	1680
	ctgtaccaga tcccacacta gagggcgctg ctggaggttc tccgagagggt tgagggtcgg	1740
	ggactgactc tgagtcgccca gtctgaccga aattgagtct ctttctggcg ggctgctggc	1800
35	ccttcttgcc gatgcccggt gaggagtcgg gggaacgctg aggtgacggc tctaccggtc	1860
	tcttctttgc aggagccgtc ttagcgcctt cctcaaccag accgagagggt tcgagaaccc	1920
	gcttcttggc ctggaagact gctcgcccga ggttgccccc aaatgacgta tcttcttgca	1980
40	gacgctcctg aaactcggcg tcggcggtgt tataccgcag gtacggggtt tcaccgcacat	2040
	tgagctgctg gtcgtaggcc ttgtcgtgct cgagggccgc tgcgtccgcc gcgttgacgg	2100
	gtccccctt gtcgagtcgg ttgaagggtc cgaggtaact gtagccagga agcaccagac	2160
45	cccgcccggt gtccctgcttt tgctggttgg ctttgggttt cggggctcca ggtttcaggt	2220
	cccaccactc gcgaatgcc tcagagagggt tgcctcagag ccaatctgga agataaccat	2280
	cggcagccat acctgattta aatcatttat tgttcaaaga tgcagtcac ccaatccaca	2340
50	ttgaccagat cgcaggcagt gcaagcgtct ggcaccttcc catgatatg atgaatgtag	2400
	cacagtttct gatacgctt tttgacgaca gaaacgggtt tagattctga caggggaaag	2460
	cactctaaac agtctttctg tccgtgagtg aagcagatat ttgaattctg attcattctc	2520
55	tcgcattgtc tgcagggaaa cagcatcaga ttcattgccc cgtgacgaga acatttgttt	2580

EP 1 310 571 B1

	tggtacctgt ctgcgtagtt gatcgaagct tccgcgtctg acgtcgatgg ctgcgcaact	2640
5	gactcgcgca cccgtttggg ctcaattata tctgcgtcac tgggggcggg tcttttcttg	2700
	gctccaccct ttttgacgta gaattcatgc tccacctcaa ccacgtaatc ctttgccac	2760
	cggaaaaagt ctttgacttc ctgcttggtg accttcccaa agtcatgac cagacggcgg	2820
10	gtgagttcaa atttgaacat cccgtcttgc aacggctgct ggtgttcgaa ggtcgttgag	2880
	ttcccgtcga tcacggcgca catgttggtg ttggagatga cgatcgcggg agtcgggtct	2940
	atctgggccg aggacttgca tttctggtcc acgcgcacct tgcttcctcc gagaatggct	3000
15	ttggcgcgact ccacgacctt ggcggtcac ttcccctcct cccaccagat caccatcttg	3060
	tcgacacagt cgttgaaggg aaagttctca ttggtccagt tgacgcagcc gtagaaaggg	3120
	cgaattc	3127

20

<210> 16

<211> 3106

<212> DNA

<213> new AAV serotype, clone 24-1

25

<400> 16

30

35

40

45

50

55

EP 1 310 571 B1

	gcggccgcga attcgccctt cgcagagacc aaagttcaac tgaaacgaat caaccggttt	60
	attgattaac aagtaattac aggttacggg tgaggtaacg ggtgccaatg gggcgaggct	120
5	cagtataaac cccttcgttg ttgacagcaa attccacatt attagacttg gcataatttg	180
	aggtgtactg aatctctgga ttccagcgtt tgctgttttc tttctgcagt tccactcga	240
	tctccacgct gacctggccg gtgctgtact gcgtgataaa tgaggcaaac ttggcaggag	300
10	taaacacctc tggaggatta gcaggtagcg ggggtgtttt gatgagaatt tgaggaggcg	360
	gggtgtttgag tccaaatccg cccatcaggg gagacgggtg aaagttgccg tccgtgtgag	420
	gaatttttggc ccagatggga ccctgcaggc acacgtcccg gttctgccag accatgccgg	480
15	gcagagcccc ctggctgttg acagtctgtg tctgggggtcc ggccgtagac gattgcaggt	540
	tgctggagac cacaccgtat tcttctgtag ccacgggatt ggtggttttg atctcctcct	600
	cgctggcat tagcacgttt tccagcgttg tcttgttggc agccccgtt ttgccaaaaa	660
20	ccagcactcc gttgatggga aagaactggg cctcgtcgtc cttgttggtg gccatggcta	720
	cgcccgggtt ggtaaatgaa tttctaccat tcagatggta tttagtggcc ccggtccagg	780
	caaagttact gttgttggtg ctgtctatgt tttttgacag tctctgctgc cgataacagg	840
25	gtccgggagc ccagttcttt gattgctcgg ccatggtgtt gggcccagcc tgatggaact	900
	gcagctccct tgtggacccc gtagtgctct ggggtccgggc caggtagtac aggtactggt	960
	cgatgagggg attcatcagc cggcttaggc tctggctgtg cacatagctg ctgtggaaag	1020
30	gcacttcctc aaagggtgtg ctgaattcaa agttattgcc cgttctcagc atctgagaag	1080

35

40

45

50

55

EP 1 310 571 B1

	gaaagtactc caggcagtag aaggaggaac gtccacaga ctgactgccg ttgttttagag	1140
	tcagatatcc gtactgagga atcatgaaca cgtccgcagg gaacggaggg aggcagccct	1200
5	ggtgcgacaga gccgaggacg tacggcagtt ggtactccga gtccgagaag acctgaatcg	1260
	tgctggtaag gttattagcg atggtcgtaa cgccgtcgtt cgtcgtgacc tccttgacct	1320
10	ggatgttgaa caacttgaac cgcagctttc tgggcccggaa tccccagttg ttgttgatga	1380
	gtcgtgccca gtcacgtggg gagaagtggc agtggaatct gttgaagtca aaatagcccc	1440
	aggggggtgct gtagctgaag aagtggttgt cgttggttagc cccgctctga cttgatatct	1500
15	gcttgtagag gtggttggtg taggtgggca gggcccagggt gcgggtgctg gtggtgatga	1560
	ctctgtcgcc cagccatgtg gaatcgcaat gccaatttcc ggaggcatta cccactccgt	1620
	cggcgccttc gttattgtct gccattgggt cgccaccgcc tgcagccatt gtaccagatc	1680
20	ccagacctga gggcgcggcg ggaggttctc cgagagggtg ggggtcgggc actgactctg	1740
	agtcgccagt ctgccc aaag ttgagcttct ttttagcggg ctgctggcct ttcttgccga	1800
	tgcccgtgga ggagtcgggg gattctatgg gtctcttctt tccaggagcc gtcttagcga	1860
25	cttcctcaac cagaccgaga ggttcgagaa cccgcttctt ggcctggaag actgctcgcc	1920
	cgaggttgcc cccaaaagac gtatcttctt gaagacgctc ctgaaactcg gcgtcggcgt	1980
	ggttgactct gaggtacggg ttgtccccct gctcgagctg cttgtcgtag gccttgctgt	2040
30	gctcgagggc cgcggcgtct gcctcggtga ccggctctcc cttgtcgagt ccgttgaagg	2100
	gtctgaggta cttgtagcca ggaagcacca gaccccgcc gtcgtcctgc ttttgctggt	2160
	tggctttggg ttctggggct ccaggtttca agtcccacca ctgcggaatg ccctcagaga	2220
35	ggttgtctc gagccaatct ggaagataac catcggcagc catacctggt ttaagtcatt	2280
	tattgctcag aaacacagtc atccagggtcc acgttgacca gatcgagggc cgagcaagca	2340
	atctcgggag cccgccccag cagatgatga atggcacaga gtttccgata cgtcctcttt	2400
40	ctgacgaccg gttgagattc tgacacgccg gggaacatt ctgaacagtc tctggtcccg	2460
	tgcgtgaagc aaatgttgaa attctgattc actctctcgc atgtcttgca gggaaacagc	2520
	atctgaagca tgccgcgctg acgagaacat ttgttttggg acctgtcggc aaagtccacc	2580
45	ggagctcctt ccgcgtctga cgtcgatgga ttccgcactg aggggcaggc ccgcttgggc	2640
	tcgcttttat ccgcgtcatc gggggcgggg ctcttggttg cccaccctt tctgacgtag	2700
	aacccatgcg ccacctcggg cacgtgatcc tgcgccagc ggaagaacct tttgacttcc	2760
50	tgctttgtca ccttgccaaa gttatgctcc agacggcggg tgggttcaaa tttgaacatc	2820
	cggctcctgca acggctgctg gtgctcgaag gtggcgctgt tcccgtcaat cagggcgac	2880
	atgttggtgt tggagggtgac ggtcacgggg gtggggctga tctgggcgga cgacttgac	2940
55	ttttggtcca cgcgcacctt gctgccgccg agaattggct tggcggactc cagcaccttg	3000

EP 1 310 571 B1

gccgtcatct tgcctcctc ccaccagatc accatcttgt cggcgcaatc gttgaaggga 3060
aagttctcat tgggtccagtt gacgcagccg tagaaagggc gaattc 3106

5

<210> 17

<211> 3102

<212> DNA

10 <213> new AAV serotype, clone 27-3

<400> 17

15

20

25

30

35

40

45

50

55

EP 1 310 571 B1

	gcggccgcga attcgccctt cgcagagacc aaagttcaac tgaaacgaat caaccggttt	60
	attgattaac aagtaattac aggttacggg tgaggtaacg ggtgccaatg gggcgaggct	120
5	cagtataaac cccttcgttg ttgacagcaa attccacatt attagacttg gcataatttg	180
	aggtgtactg aatctctgga ttccagcgtt tgctgttttc tttctgcagt tccactcga	240
	tctccacgct gacctggccg gtgctgtact gcgtgataaa tgaggcaaac ttggcaggag	300
10	taaacacctc tggaggatta gcaggtagcg ggggtgtttt gatgagaatt tgaggaggcg	360
	ggtgtttgag tccaaatccg cccatcaggg gagacgggtg aaagttgccg tccgtgtgag	420
	gaatttcggc ccagatggga ccctgcaggt acacgtcccg gttctgccag accatgccgg	480
15	gcagagcccc ctggctgttg acagtctgtg tccgggggcc ggccgtagac gattgcaggt	540
	tgctggagac cacaccgtat tcttctgtag ccacgggatt ggtggttttg atctcctcct	600
	cgtcggtcac tagcacgttt tccagcgttg tcttggtggc agcccccggt ttgccaaaaa	660
20	ccagcactcc gttgatggga aggaactggc cctcgtcgtc cttgttggtg gccatggcta	720
	cgcccggggt ggttaatgaa tttctaccat tcagatggta tttagtggcc ccggtccagg	780
	caaagttact gttgttggtg ctgtctatgt tttttgacag tctctgctgc cgataacagg	840
25	gtccgggcag ccagttcttt gattgctcgg ccacgggtgtt gggcccagcc tgatggaact	900
	gcagctccct tgtggacccc gtagtgctct ggggtccggc caggtagtac aggtactggt	960
	cgatgagggg attcatcagc cgggtccaggc tctggctgtg cgcatagctg ctgtggaaag	1020
30	gcacttcctc aaagggtgtag ctgaattcaa agttattgcc cgttctcagc atctgagaag	1080
	gaaagtactc caggcagcag aaggaggaac gtcccacaga ctgactgccg ttgttttagag	1140
	tcagatatcc gtactgagga atcatgaaca cgtccgcagg gaacggaggg aggagccct	1200
35	ggtgcgcaga gccgaggacg tacggcagtt ggtactccga gtccgagaag acctgaatcg	1260
	tgctggtaag gttattagcg atggtcgtaa cgccgtcgtt cgtcgtgacc tccttgacct	1320
	ggatgttgaa caacttgaa cgcagctttc tgggocggaa tcccagttg ttgttgatga	1380
40	gtcgtgccca gtcacgtggt gagaagtggc agtggaatct gttgaagtca aaatagcccc	1440
	aggggggtgct gtagccgaag aagtgggtgt cgttggttagc cccgctctga cttgatatct	1500
	gcttgtagag gtggttggtg taggtgggca gggcccagggt gcgggtgctg gtggtgatga	1560
45	ctctgtcgcc cagccatgtg gaatcgcaat gccaatttcc ggaggcatta cccactccgt	1620

50

55

EP 1 310 571 B1

5
 10
 15
 20
 25
 30
 35
 40
 45
 50
 55

cggcgcccttc gttattgtct gccattggtg cgccaccgcc tgcagccatt gtaccagatc 1680
 ccagacctga gggcgcgggc ggaggttctc cgagaggttg ggggtcgggc actgactctg 1740
 agtcgccagt ctgccc aaag ttgagcttct ttttagcggg ctgctggcct ttcttgccga 1800
 tgcccggtga ggagtcgggg gattctatgg gtctcttctt tccggaagcc gtcttagcgc 1860
 cttcctcaac cagaccgaga ggttcgagaa cccgcttctt ggcttggaag actgctcgcc 1920
 cgaggttgcc cccaaaagac gtatcttctt gaagacgctc ctgaaactcg gcgtcggcgt 1980
 ggttgactct gaggtacggg ttgtccccct gctcgagctg cttgtcgtag gccttgctcg 2040
 gctcgagggc cgcggcgtct gcctcggtga ccggctctcc cttgtcgagt ccgttggaagg 2100
 gtccgaggtg cttgtagcca ggaagcacca gaccccgccc gtcgtcctgc ttttgctggt 2160
 tggtcttggg tttcggggct ccaggtttca agtcccacca ctgcggaatg ccctcagaga 2220
 ggttgctctc gagccaatct ggaagataac catcggcagc catacctggt ttaagtcatt 2280
 tattgctcag aaacacagtc atccagggtc acgttgacca gatcgaggc cgagcaagca 2340
 atctcgggag cccgccccag cagatgatga atggcacaga gtttccgata cgtcctcttt 2400
 ctgacgaccg gttgagattc tgacacgccg gggaaacatt ctgaacagtc tctggtcccg 2460
 tgcgtgaagc aaatgttgaa attctgattc attctctcgc atgtcttgca gggaaacagc 2520
 atctgaagca tgcccgcgtg acgagaacat ttgttttggg acctgtcggc aaagtccacc 2580
 ggagctcctt ccgcgtctga cgtcgatgga tccgcgactg aggggcaagc ccgcttgggc 2640
 tcgcttttat ccgcgtcctc gggggcgggg ctcttggttg ctcaccctt tctgacgtag 2700
 aactcatgcg ccacctcggg cacgtgatcc tgcgccagc ggaagaactc tttgacttcc 2760
 tgctttgtca ccttgccaaa gtcattgctc agacggcggg tgagttcaaa tttgaacatc 2820
 cggctcttgta acggctgctg gtgctcgaag gtggtgctgt tcccgtaac caccgagcac 2880
 atgttggtgt tggaagtga gatcacggg gtgggatcga tctgggaggc cgaactgcac 2940
 ttttggtcca cgcgcacctt gctgcgcgcg agaatggcct tggcggactc cagcaccttg 3000
 gccgtcatct tgccctctc ccaccagatc accatcttgt cgacgcaatc gttgaaggga 3060
 aagttctcat tgggtccagtt gacgcagccg aaggcgcaat tc 3102
 <210> 18
 <211> 3106
 <212> DNA
 <213> new AAV serotype, clone 7-2
 <400> 18
 gcggccgcga attcgccctt cgagagacc aaagttcaac tgaaacgaat cagccggttt 60
 attgattaac aagtaattac aggttacggg tgaggtaacg ggtgccaatg gggcgaggct 120
 cagtataaac cccttcgttg ttgacagcaa attccacatt attagacttg gcataatttg 180

EP 1 310 571 B1

	aggtgtactg aatctctgga ttccagcggt tgctgttttc tttctgcagt tcccactcga	240
	tctccacgct gacctggccg gtgctgtact gcgtgataaa tgaggcaaac ttggcaggag	300
5	taaacacctc tggaggatta gcaggtagcg ggggtgtttt gatgagaatt tgaggaggcg	360
	gggtgtttgag tccaaatccg cccatcaggg gagacgggtg aaagttgccg tccgtgtgag	420
	gaattttggc ccagatggga ccctgcaggt acacgtcccg gttctgccag accatgccgg	480
10	gcagagcccc ctggctgttg acagtctgtg tctgggggtcc ggccgtagac gattgcaggt	540
	tgctggagac cacaccgtat tcttctgtag ccacgggatt ggtgggtttg atctcctcct	600
	cgctggcat tagcacgttt tccagcggtg tcttggtggc agccccgtt ttgccaaaaa	660
15	ccagcactcc gttgatggga aagaactggg cctcgtcgtc cttgttggtg gccatggcta	720
	cgcgcgggtt ggttaatgaa tttctacatc tcagatggta tttagtggcc ccggtccagg	780
	caaagttact gttgttggtg ctgtctatgt ttttgacag tctctgctgc cgataacagg	840
20	gtccgggcag ccagttcttt gattgctcgg ccatggtgtt gggcccagcc tgatggaact	900
	gcagctccct tgtggacccc gtagtgctct ggggtccggg caggtagtac aggtactggt	960
	cgatgagggg attcatcagc cgggtccaggc tctggctgtg cgcatagctg ctgtggaaag	1020
25	gcacttcctc aaagggtgtag ctgaattcaa agttatcgcc cgttctcagc atctgagaag	1080
	gaaagtactc caggcagtag aaggaggaaac gtcccacaga ctgactgccg ttgttttagag	1140
	tcagatatcc gtactgagga atcatgaaca cgtccgcagg gaacggaggg aggcagccct	1200
30	gggtgcgcaga gccgaggacg tacggcaggt ggtactccga gtccgagaag acctgaatcg	1260
	tgctggtaag gttattagcg atggtcgtaa cgccgtcgtt cgtcgtgacc tccttgacct	1320
	ggatgttgaa caacttgaac cgcagctttc tgggcccggaa tccccagttg ttgttgatga	1380
35	gtcgtgcca gtcacgtggt gagaagtggc agtggaatct gttgaagtca aaatagcccc	1440
	aggggggtgct gtagccgaag aagtgggtgt cgttggtagc cccgctctga cttgatattc	1500
	gcttgtagag gtggttggtg taggtgggca gggcccaggt gcgggtgctg gtggtgatga	1560
40	ctctgtcgcc cagccatgtg gaatcgcaat gccaatcttc ggaggcatta cccactccgt	1620
	cggcgccttc gttattgtct gccattggtg cgccaccgcc tgcagccatt gtaccagatc	1680
	ccagacctga gggcgcgggc ggagggtctc cgagagggtg ggggtcgggc actgactctg	1740
45	agtcgccagt ctgcccgaag ttgagcttct ttttagcggg cggctggccg ttcttgccga	1800
	tgcccgtgga ggagtcgggg gattctatgg gtctcttctt tccaggagcc gtcttagcgc	1860
	cttctcaaac cagaccgaga ggttcgagaa ccgcttctt ggccctggaag actgctcgcc	1920
50	cgaggttgcc cccaaaagac gtatcttctt gaagacgctc ctgaaactcg gcgtcggcgt	1980
	ggttgtactt gaggtacggg ttgtccccct gctcgagctg cttgtcgtag gccttgctgt	2040
55	gctcgagggc cgcggcgtct gcctcgttga ccggtctctc cttgtcgtgt ccgttgaagg	2100

EP 1 310 571 B1

	gtccgaggta cctgtagcca ggaagcacca gaccccggcc gtcgtcctgc ttttgctggt	2160
5	tggttttggg tttcggggct ccagggtttca agtcccacca ctgcggaatg ccctcagaga	2220
	gggtgcccctc gagccaatct ggaagataac catcggcagc catacctggt ttaagtcatt	2280
	tattgctcag aaacacagtc atccagggtcc acgttggcca gatcgcaggc cgagcaagca	2340
10	atctcgggag cccgccccag cagatgatga atggcacaga gtttccgata cgtcctcttt	2400
	ctgacgaccg gttgagattc tgacacgccg gggaaacatt ctgaacagtc tctggtcccg	2460
	tgcgtgaagc aaatgttgaa attctgattc attctctcgc atgtcttgca ggggaacagc	2520
15	atctgaagca tgcccgcgtg acgagaacat ttgttttggg acctgtcggc aaagtccacc	2580
	ggagctcctt ccgcgtctga cgtcgaatga tccgcgactg aggggcaggc ccgcttgggc	2640
	tcgcttttat ccgcgtcatc gggggcgggt ctcttggttg ctcaccctt tctgacgtag	2700
20	aactcatacg ccacctcggg cacgtgatcc tgcgccagc ggaagaactc tttgacttcc	2760
	tgctttgtca ctttgccaaa gtcattgctcc agacggcggg tgagttcaa tttgaacatc	2820
	cggctcttgta acggctgctg gtgctcgaag gtgggtgctgt tcccgtcaat cacggcgcac	2880
25	atgttggtgt tggaagtgc gatcacggg gtgggatcga tctgggcgga cgacttgcac	2940
	ttttggtcca cgcgcacctt gctgccgccg agaattggct tggcggactc cagcaccttg	3000
	gccgtcatcc tgccctcctc ccaccagatc accatcttgt cgacgcaatc gttgaagggg	3060
30	aagttctcat tgggtccagtt gacgcagccg tagaaagggc gaattc	3106

<210> 19

<211> 3105

<212> DNA

<213> new AAV serotype, clone C1

<400> 19

EP 1 310 571 B1

	gaattcgccc ttgctgctgc aactggacca atgagaactt tcccttcaac gattgcgtcg	60
	acaagatggt gatctggtgg gaggagggca agatgaccgc caaggctcgtg gagtccgcca	120
5	aggccattct gggcggaagc aagggtgcgcg tggacaaaa gtgcaagtca tcggcccaga	180
	tcgacccac gcccgatgatc gtcacctcca acaccaacat gtgcgccgtg atcgacggga	240
	acagcaccac cttcgagcac cagcagccgc tgcaggaccg catgttcaag ttcgagctca	300
10	cccgccgtct ggagcacgac tttggcaagg tgaccaagca ggaagtcaaa gagttcttcc	360
	gctgggctca ggatcacgtg actgaggtgg cgcattgagtt ctacgtcaga aagggcggag	420
	ccaccaaaaag acccgcccc agtgacgcgg atataagcga gcccaagcgg gcctgcccct	480
15	cagttgcgga gccatcgacg tcagacgcgg aagcaccggt ggactttgcg gacaggtacc	540
	aaaacaaatg ttctcgtcac gcgggcatgc ttcagatgct gtttcctgc aagacatgcg	600
	agagaatgaa tcagaatttc aacgtctgct tcacgcacgg ggtcagagac tgctcagagt	660
20	gcttccccgg cgcgtcagaa tctcaaccgg tcgtcagaaa aaagacgtat cagaaactgt	720

25

30

35

40

45

50

55

EP 1 310 571 B1

	gcgcgattca	tcattctgctg	gggcggggcac	ccgagattgc	gtgttcggcc	cgcgatctcg	780
	tcaacgtgga	cttgatgac	tgtgtttctg	agcaataaat	gacttaaacc	aggtatggct	840
5	gctgacgggt	atcttccaga	ttggctcgag	gacaacctct	ctgagggcat	tcgcgagtgg	900
	tgggacctga	aacctggagc	ccccaaagccc	aaggccaacc	agcagaagca	ggacgacggc	960
10	cgggggtctg	tgcttcctgg	ctacaagtac	ctcggaccct	tcaacggact	cgacaagggg	1020
	gagcccgtca	acgcggcgga	cgcagcggcc	ctcgagcacg	acaaggccta	cgaccagcag	1080
	ctcaaagcgg	gtgacaatcc	gtacctgcgg	tataaccacg	ccgacgccga	gtttcaggag	1140
15	cgtctgcaag	aagatacgtc	ttttgggggc	aacctcgggc	gagcagtctt	ccaggccaag	1200
	aagaggggtac	tcgaacctct	gggcctgggt	gaagaagggtg	ctaagacggc	tcctggaaaag	1260
	aagagaccgt	tagagtcacc	acaagagccc	gactcctcct	caggaatcgg	caaaaaaggc	1320
20	aaacaaccag	caaaaaagag	actcaacttt	gaagaggaca	ctggagccgg	agacggaccc	1380
	cctgaaggat	cagataccag	cgccatgtct	tcagacattg	aatgctgtgc	agcaccgggc	1440
	ggaaatgctg	tcgatgcggg	acaaggttcc	gatggagtgg	gtaatgcctc	gggtgattgg	1500
25	cattgcgatt	ccacctggtc	tgagggcaag	gtcacaacaa	cctcgaccag	aacctgggtc	1560
	ttgccacct	acaacaacca	cttgtacctg	cggctcggaa	caacatcaaa	cagcaacacc	1620
	tacaacggat	tctccacccc	ctggggatac	tttgacttta	acagattcca	ctgtcacttc	1680
30	tcaccacgtg	actggcaaag	actcatcaac	aacaactggg	gactacgacc	aaaagccatg	1740
	cgcgttaaaa	tcttcaatat	ccaagttaag	gaggtcacia	cgtcgaacgg	cgagactacg	1800
	gtcgctaata	accttaccag	cacggttcag	atatttgccg	actcgtcgta	tgagctcccg	1860
35	tacgtgatgg	acgttgga	agagggaagt	ctgtctcctt	tccccaatga	cgtcttcatg	1920
	gtgcctcaat	atggctactg	tggcattgtg	actggcgaaa	atcagaacca	gacggacaga	1980
	aatgctttct	actgcctgga	gtattttcct	tcacaaatgc	tgagaactgg	caataacttt	2040
40	gaaatggctt	acaactttgg	gaagggtgcc	ttccactcaa	tgtatgctta	cagccagagc	2100
	ccggacagac	tgatgaatcc	cctcctggac	cagtacctgt	ggcacttaca	gtcgaccacc	2160
	tctggagaga	ctctgaatca	aggcaatgca	gcaaccacat	ttggaaaaat	caggagtggg	2220
45	gactttgcct	tttacagaaa	gaactggctg	cctgggcctt	gtgttaaaca	gcagagactc	2280
	tcaaaaactg	ccagtcaaaa	ttacaagatt	cctgccagcg	ggggcaacgc	tctgttaaag	2340
	tatgacaccc	actatacctt	aaacaaccgc	tgagcaaca	tagcgcctgg	acctccaatg	2400
50	gcaacagctg	gaccttcaga	tggggacttc	agcaacgccc	agctcatctt	ccctggacca	2460
	tcagtcaccg	gaaacacaa	aacctcagca	aacaatctgt	tgtttacatc	agaagaagaa	2520
	attgctgcca	ccaacccaag	agacacggac	atgtttggtc	agattgctga	caataatcag	2580
55	aatgctacaa	ctgctcccat	aaccggcaac	gtgactgcta	tgggagtgtc	tcctggcatg	2640

EP 1 310 571 B1

	gtgtggcaaa acagagacat ttactaccaa gggccaatTTT gggccaagat cccacacgcg	2700
5	gacggacatt tTcatccttc accgctaatt ggcggTTTTg gactgaaaca tccgcctccc	2760
	cagatatTTta tcaaaaaacac ccccgTacct gccaatcctg cgacaacctt cactgcagcc	2820
	agagtggact ctttcatcac acaatacagc accggccagg tcgctgttca gattgaatgg	2880
10	gaaatcgaaa aggaacgctc caaacgctgg aatcctgaag tgcagtttac ttcaaactat	2940
	gggaaccagt cttctatgtt gtgggctccc gatacaactg ggaagtatac agagccgcgg	3000
	gttattggct ctcgttatTTt gactaatcat ttgtaactgc ctagttaatc aataaaccgt	3060
15	gtgattcgTt tcagttgaac tttggTctct gcgaagggcg aattc	3105

<210> 20

<211> 3105

20 <212> DNA

<213> new AAV serotype, clone C3

<400> 20

25

30

35

40

45

50

55

EP 1 310 571 B1

	gaattcgccc ttgctgcgtc aactggacca atgagaactt tcccttcaac gattgcgtcg	60
	acaagatggt gatctggtgg gaggagggca agatgaccgc caaggtcgtg gagtccgcca	120
5	aggccattct gggcggaagc aaggtgcgcg tggacaaaa gtgcaagtca tcggcccaga	180
	tcgaccccac gcccgatgac gtcacctcca acaccaacat gtgcgccgtg atcgacggga	240
	acagcaccac cttcgagcac cagcagccgc tgcaggaccg catgttcaag ttcgagctca	300
10	cccgccgtct ggagcacgac tttggcaagg tgaccaagca ggaagtcaaa gagttcttcc	360
	gctgggctca ggatcacgtg actgaggtgg cgcattgagt ctacgtcaga aagggcggag	420
	ccaccaaaag acccgccccc agtgacgcgg atataagcga gcccaagcgg gcctgccct	480
15	cagttgcgga gccatcgacg tcagacgcgg aagcaccggt ggactttgcg gacaggtacc	540
	aaaacaaatg ttctcgtcac gcgggcatgc ttcagatgct gtttccttgc aagacatgcg	600
	agagaatgaa tcagaatttc aacgtctgct tcacgcacgg ggtcagagac tgctcagagt	660
20	gcttccccgg cgcgtcagaa tctcaaccgg tcgtcagaaa aaagacgtat cagaaactgt	720
	gcgcgattca tcatctgctg gggcgggcac ccgagattgc gtgttcggcc tgcgatctcg	780
	tcaacgtgga cttggatgac tgtgtttctg agcaataaat gacttaaacc aggtatggct	840
25	gctgacgggt atcttccaga ttggctcgag gacaacctct ctgaggcat tcgcgagtgg	900
	tgggacctga aacctggagc ccccaagctc aaggccaacc agcagaagca ggacgacggc	960
	cggggtctgg tgcttcttgg ctacaagtac ctcggaacct tccacggact cgacaagggg	1020
30	gagcccgctc acgcggcgga cgcagcggcc ctcgagcacg acaaggccta cgaccagcag	1080
	ctcaaagcgg gtgacaatcc gtacctgcgg tataaccacg ccgacgccga gtttcaggag	1140
	cgtctgcaag aagatacgtc ttttgggggc aacctcgggc gagcagtctt ccaggccaag	1200
35		
40		
45		
50		
55		

EP 1 310 571 B1

	aagaggggtac tcgaaccact gggcctgggt gaagaagggtg ctaagacggc tcctggaaag	1260
	aagagaccgt tagagtcacc acaagagccc gactcctcct caggaatcgg caaaaaaggc	1320
5	aaacaaccag ccaaaaagag actcaacttt gaagaggaca ctggagccgg agacggaccc	1380
	cctgaaggat cagataccag cgccatgtct tcagacattg aaatgcgtgc agcaccgggc	1440
10	ggaaatgctg tcgatgcggg acaagggttc gatggagtgg gtaatgcctc gggtgattgg	1500
	cattgcgatt ccacctgggtc tgagggcaag gtcacaacaa cctcgaccag aacctgggtc	1560
	ttgccacact acaacaacca cttgtacctg cggctcggaa caacatcaaa cagcaacacc	1620
15	tacaacggat tctccacccc ctggggatac ttgacttta acagattcca ctgtcacttc	1680
	tcaccacgtg actggcaaag actcatcaac aacaactggg gactacgacc aaaagccatg	1740
	cgcgttaaaa tcttcaatat ccaagttaag gaggtcacia cgtcgaacgg cgagactacg	1800
20	gtcgctaata accttaccag cacggttcag atatttgcgg actcgtcgta tgagctcccg	1860
	tacgtgatgg acgctggaca agagggaagt ctgcctcctt tccccaatga cgtcttcatg	1920
	gtgcctcaat atggctactg tggcattgtg actggcgaaa atcagaacca gacggacaga	1980
25	aatgctttct actgcctgga gtattttcct tcacaaatgc tgagaactgg caataacttt	2040
	gaaatggctt acaactttga gaagggtgccc ttccactcaa tgtatgctca cagccagagc	2100
	ctggacagac tgatgaatcc cctcctggac cagtacctgt ggcacttaca gtcgaccacc	2160
30	tctggagaga ctctgaatca aggcaatgca gcaaccacat ttggaaaaat caggagtggg	2220
	gactttgcct ttacagaaa gaactggctg cctgggcctt gtgttaaaca gcagagattc	2280
	tcaaaaactg ccagtcaaaa ttacaagatt cctgccagcg ggggcaacgc tctgttaaag	2340
35	tatgacaccc actatacctt aaacaaccgc tggagcaaca tagcgcttgg acctccaatg	2400
	gcaacagctg gaccttcaga tggggacttc agcaacgccc agctcatctt ccctggacca	2460
	tcagtcaccg gaaacacaa aacctcagca aacaatctgt tgtttacatc agaaggagaa	2520
40	attgctgcca ccaaccgaag agacacggac atgtttgggt agattgctga caataatcag	2580
	aatgctacaa ctgctcccat aaccggcaac gtgactgcta tgggagtgtt tcctggcatg	2640
	gtgtggcaaa acagagacat ttactaccaa gggccaattt gggccaagat cccacacgcg	2700
45	gacggacatt ttcctccttc accgctaatt ggcggttttg gactgaaaca tccgcctccc	2760
	cagatattta tcaaaaacac ccccgctact gccaatcctg cgacaacctt cactgcagcc	2820
	agagtggact ctttcatcac acaatacagc accggccagg tcgctgttca gattgaatgg	2880
50	gaaatcgaaa aggaacgctc caaacgccgg aatcctgaag tgcagtttac ttcaaactat	2940
	gggaaccagt cttctatgtt gtgggctccc gatacaactg ggaagtatac agagccgcg	3000
	gttattggct ctcgttattt gactaatcat ttgtaactgc ctagttaatc aataaaccgt	3060
55	gtgattcggt tcagttgaac tttgggtctt gcgaaggcg aattc	3105

<210> 21

EP 1 310 571 B1

<211> 3105

<212> DNA

<213> new AAV serotype, clone C5

5

<400> 21

	gaattcgccc	ttcgcagaga	ccaaagttca	actgaaacga	atcacacggt	ttattgatta	60
10	actaggcagt	tacaaatgat	tagtcaaata	acgagagcca	ataaccgcg	gctctgtata	120
	cttcccagtt	gtatcgggag	cccacaacat	agaagactgg	ttcccacagt	ttgaagtaaa	180
	ctgcacttca	ggattccagc	gtttggagcg	ttccttttcg	atttcccatt	caatctgaac	240
15	agcgacctgg	ccggtgctgt	attgtgtgat	gaaagagtcc	actctggctg	cagtgaaggt	300
	tgtcgcagga	taggcaggta	cgggggtgtt	tttgataaat	atctggggag	gcggatgttt	360
	cagtccaaaa	ccgccaat	gcggtgaagg	atgaaaatgt	ccgtccgcgt	gtgggatctt	420
20	ggcccaaatt	ggcccttgg	agtaaatgtc	tctgttttgc	cacaccatgc	caggaagcac	480
	tcccatagca	gtcacgttgc	cggttatggg	agcagttgta	gcattctgat	tattgtcagc	540
	aatctgacca	aacatgtccg	tgtctcttgg	gttgggtggc	gcaatttctt	cttctgatgt	600
25	aaacaacaga	ttgtttgctg	aggttgttgt	gtttccggtg	actgatggtc	caggaagat	660
	gagctgggcg	ttgctgaagt	ccccatctga	aggtccagct	gttgccattg	gaggtccagg	720
	cgctatgttg	ctccagcggt	tgtttaaggt	atagtgggtg	tcatacttta	acagagcggt	780
30	gccccgcgtg	gcaggaatct	tgtaattttg	actggcagtt	tttgagaatc	tctgctgttt	840
	aacacaaggc	ccaggcagcc	agttctttct	gtaaaaggca	aagtctccac	tcctgatttt	900
	tccaaatgtg	gttgctgcat	tgccttgatt	cagagtctct	ccagagggtg	tcgactgtaa	960
35	gtgccacagg	tactggtcca	ggaggggatt	catcagtcgc	tccaggctct	ggctgtgagc	1020
	atacattgag	tggaacggca	ccttctcaaa	gttgtaagcc	gtttcaaagt	tattgccagt	1080
	tctcagcatt	tgtgaaggaa	aatactccag	gcagtagaaa	gcatttctgt	ccgtctgggt	1140
40	ctgatttttcg	ccagtcacaa	tgccacagta	gccatattga	ggcaccatga	agacgtcatt	1200
	ggggaaagga	ggcagacttc	cctcttgtcc	agcgtccatc	acgtacggga	gtccatacga	1260
	cgagtccgca	aatatctgaa	ccgtgctgg	aaggttatta	gcgaccgtag	tctcgccgtt	1320
45	cgacgttgtg	acctccttaa	cttggtatatt	gaagatttta	acgcgcatgg	cttttggtcg	1380
	tagtccccag	ttgttgttga	tgagtctttg	ccagtcacgt	ggtgagaagt	gacagtggaa	1440
	tctgttaaag	tcaaagtatc	cccaggggg	ggagaatccg	ttgtaggtgt	tgctgtttga	1500
50	tggtgttccg	agccgcaggt	acaagtgggt	gttgtaggtg	ggcaagacc	aggttctgg	1560
	cgagggttgt	gtgaccttgc	cctcagacca	ggtggaatcg	caatgccaat	caccgaggc	1620
	attaccact	ccatcggaac	cttgtcccgc	atcgacagca	tttccgcccg	gtgctgcacg	1680
55	catttcaatg	tctgaagaca	tggcgtgg	atctgatcct	tcagggggtc	cgtctccggc	1740

EP 1 310 571 B1

	tccagtgtcc tcttcaaagt tgagtctctt tttggctggg tgtttgcctt ttttgccgat	1800
	tcctgaggag gagtcgggct cttgtggtga ctctaacggg ctcttctttc caggagccgt	1860
5	cttagcacct tcttcaacca ggcccagagg ttcgagtacc ctcttcttgg cctggaagac	1920
	tgctcgcccc aggttgcccc caaaagacgt atcttcttgc agacgctcct gaaactcggc	1980
10	gtcggcgtagg ttataaccga ggtacggatt gtcaccgct ttgagctgct ggtcgtaggc	2040
	cttgctcgtgc tcgaggggcg ctgctgcgc cgcggtgacg ggctccccct tgtcgagtcc	2100
	gttgaagggg ccgaggtact cgtagccagg aagcaccaga ccccgggcgt cgtcctgctt	2160
15	ctgctgggtg gccttgggct tgggggctcc aggtttcagg tcccaccact cgcgaatgcc	2220
	ctcagagagg ttgtcctcga gccaatctgg aagataaccg tcagcagcca tacctggttt	2280
	aagtcattta ttgctcagaa acacagtcac ccaagtcac gttgacgaga tcgcaggccg	2340
20	aacacgcaat ctcggtgccc cgccccagca gatgatgaat cgcgcacagt ttctgatacg	2400
	tcttttttct gacgacgggt tgagattctg acgcgccggg gaagcactct gagcagtctc	2460
	tgaccccggt cgtgaagcag acgttgaaat tctgattcat tctctcgcac gtcttgacgg	2520
25	gaaacagcat ctgaagcatg ccgcggtgac gagaacattt gttttggtac ctgtccgcaa	2580
	gggccaccgg tgccttcgcg tctgacgtcg atggctccgc aactgagggg caggcccgtc	2640
	tgggctcgct tatatccgcg tcaactgggg cggttctttt ggtggctccg ccttttctga	2700
30	cgtagaactc atgcgccacc tcagtcacgt gatcctgagc ccagcggaag aactctttga	2760
	cttctgctt ggtcaccttg ccaaagtcgt gctccagacg gcgggtgagc tcgaacttga	2820
	acatgcggtc ctgcagcggc tgctggtgct cgaaggtagt gctgttcccg tcgatcacgg	2880
35	cgcacatggt ggtggtggag gtgacgatca cgggcgtggg gtcgatctgg gccgatgact	2940
	tgcacttttg gtccacgcgc accttgcttc cgcccagaat ggcttggcg gactccacga	3000
	ccttggcggg catcttgccc tctcccacc agatcaccat cttgtcgacg caatcgttga	3060
40	agggaaagtt ctcatgggtc cagttgacgc agcaagggcg aattc	3105

<210> 22

<211> 3094

<212> DNA

45 <213> new AAV serotype, clone F1

<400> 22

50	gaattcgccc ttgctgcgtc aactggacca agagaacttt cccttcaacg attgcgtcga	60
	caagatggtg atctggtggg aggagggcaa gatgacggcc aaggctcgtg agtccgccaa	120
	agccattctg ggcggaagca aggtgcgcgt cgaccaaag tgcaagtcct cggcccagat	180
55	cgatcccacc cccgtgatcg tcacctcaa caccaacatg tgcgccgtga tcgacgggaa	240
	cagcaccacc ttcgagcacc agcagccgtt gcaggaccgg atgttcaaatt ttgaactcac	300

EP 1 310 571 B1

	ccgccgtctg gaacacgact ttggcaaggt gaccaagcag gaagtcaaag agttcttccg	360
5	ctgggctagt gatcacgtga ctgaggtgac gcatgagttc tacgtcagaa agggcggagc	420
	cagcaaaaga cccgcccccg atgacgcgga tataagcgag cccaagcggg cctgtccctc	480
	agtcacggac ccatcgacgt cagacgcgga aggagctccg gtggactttg ccgacaggta	540
10	ccaaaacaaa tgttctcgtc acgcgggcat gcttcagatg ctgtttccct gcaaaacgtg	600
	cgagagaatg aatcagaatt tcaacatttg cttcacgcac ggggtcagag actgtttaga	660
	atgtttcccc ggcggtgcag aatctcaacc ggtcgtcaga aaaaagacgt atcggaagct	720
15	gtgtgcgatt catcatctgc tggggcgggc acccgagatt gcttgctcgg cctgcgacct	780
	gggtcaacgtg gacctggacg actgtgtttc tgagcaataa atgacttaaa ccgggtatgg	840
	ctgccgatgg ttatcttcca gattggctcg aggacaacct ctctgagggc attcgcgagt	900
20	gggtgggacct gaaacctgga gccccgaaac ccaaagccaa ccagcaaaag caggacgacg	960
	gccgggggtct ggtgcttccct ggctacaagt acctcggacc cttcaacgga ctcgacaagg	1020
	gggagcccggt caacgcggcg gacgcagcgg ccctcgagca cgacaaggcc tacgaccagc	1080
25	agctcaaagc ggggtgacaat ccgtacctgc ggtataacca cgccgacgcc gagtttcagg	1140
	agcgtctgca agaagatacg tcatttgggg gcaacctcgg gcgagcagtc ttccaggcca	1200
	agaagcgggt tctcgaacct ctcggtctgg ttgaggaagg cgctaagacg gctcctggaa	1260
30	agaagagacc catagactct ccagactcct ccacgggcat cggcaaaaaa ggccagcagc	1320
	ccgctaaaaa gaagctcaat tttggtcaga ctggcgactc agagtcagtc cccgaccctc	1380
	aacctcttgg agaacctcca gcagcgccct ctagtgtggg atctggtaca atggctgcag	1440
35	gcggtggcgc accaatggca gacaataacg aagggtgccg cggagtgggt aatgcctcag	1500
	gaaattggca ttgcgattcc acatggctgg gcgacagagt catcaccacc agcaccagaa	1560
	cctggggccct ccccacctac aacaaccacc tctacaagca aatctccagc agcagctcag	1620
40	gagccaccaa tgacaaccac tacttcggct acagcaccct ctgggggtat tttgacttta	1680
	acagattcca ctgccacttc tcaccacgtg actggcagcg actcatcaac aacaactggg	1740
	gattccggcc caagaagctg cggttcaagc tcttcaacat ccagggtcaag gaggtcacia	1800
45	cgaatgacgg cgtcacgacc atcgctaata accttaccag cacgggtcag gtcttctcgg	1860
	actcggaata ccagctgccg tacgtcctcg gctctgcgca ccagggtcgc ctgcctccgt	1920
	tcccggcgga cgtcttcatg attcctcagt acggctacct gactctgaac aacggcagcc	1980
50	aatcggtggg ccgttccctc ttctactgcc tggaatatct cccctctcaa atgctgagaa	2040
	cgggcaacaa ctttgagttc agttacagct tcgaggacgt gcctttccac agcagctacg	2100
	cgcacagcca gagcctagac cggctgatga accctctcat cgaccagtac ctgtactacc	2160
55	tggcccggac ccagagcacc acgggttcca ccagggaact gcaatttcat caagctgggc	2220

EP 1 310 571 B1

	ccaatactat ggccgagcag tcaaagaact ggctgcctgg accctgctat aggcaacagg	2280
	gactgtcaaa gaacttggac tttacaaca acagcaatth tgcttggaat gctggcacta	2340
5	aatatcatct gaatggcaga aactctttga ccaatcctgg cattcccatg gcaaccaaca	2400
	aggatgatga ggaccagttc tttcccatca acgggggtact ggthttttggc aagacggggag	2460
	ctgccaacaa aactacgctg gaaaacgttc tgatgaccag cgaggaggag atcaagacca	2520
10	ctaaccctgt ggctacagaa gaatacgggtg tggctctccag caacctgcag ccgtctacag	2580
	ccgggcctca atcacagact atcaacagcc agggagcact gcctggcatg gtctggcaga	2640
	accgggacgt gtatctgcag ggtcccatct gggccaaaat tcctcacacg gatggcaact	2700
15	ttcaccgctc tcctctgatg ggcggttttg gactcaaaca cccgcctcca cagatcctga	2760
	tcaaaaacac acctgtacct gctaatactc cggagggtgt tactcctgcc aagtttgcct	2820
	ccttcatcac gcagtacagc accggacaag tcagcgtgga aatcgagtgg gagctgcaga	2880
20	aagaaaacag caagcgctgg aaccacagaa ttcagtatac ttccaattat gccaaagtcta	2940
	ataatgttga atttgctgtg aacctgatg gtgtttatac tgagcctcgc cccattggca	3000
	ctcgttacct cccccgtaat ctgtaattgc ttgttaatca ataaaccggt tgattcgttt	3060
25	cagttgaact ttggtctctg cgaagggcga attc	3094

30 <210> 23
 <211> 3095
 <212> DNA
 <213> new AAV serotype, clone F3

35 <400> 23

40

45

50

55

EP 1 310 571 B1

	gaattcgccc ttcgcagaga ccaaagttca actgaaacga atcaaccggt ttattgatta	60
	acaagcaatt acagattacg ggtgaggtaa cgagtgccaa tggggcgagg ctcaagtataa	120
5	acaccatcag gggtcacagc aaattcaaca ttattagact tggcataatt ggaagtatac	180
	tgaatttctg gggtccagcg cttgctgttt tctttctgca gctccactc gatttccacg	240
	ctgacttgct cggtgctgta ctgcgtgatg aaggaggcaa acttggcagg agtaaacc	300
10	tccggaggat tagcaggtac aggtgtgttt ttgatcagga tctgtggagg cgggtgtttg	360
	agtccaaaac cgcccatcag aggagacggg tgaaagtgc catccgtgtg aggaattttg	420
	gcccagatgg gaccctgcag atacacgtcc cggttctgcc agaccatgcc aggcagtgct	480
15	ccctggctgt tgatagtctg tgattgaggc ccggctgtag acgactgcag gttgctggag	540
	accacaccgt attcttctgt agccacaggg ttagtggctc tgatctcctc ctgctggtc	600
	atcagaacgt tttccagcgt agttttgttg gcagctcccg tcttgccaaa aaccagtacc	660
20	ccgttgatgg gaaagaactg gtcctcatca tccttgttgg ttgccatggg aatgccagga	720
	ttggtcaaag agtttctgcc attcagatga tatttagtgg cagcagtcca ggcaaaattg	780
25		
30		
35		
40		
45		
50		
55		

EP 1 310 571 B1

	ctgttggtgt taaagtccaa gttcttttgac agtctctgtt gcctatagca ggggccagggc	840
5	agccagttct ttgactgctc ggccatagta ttggggcccag cttgatgaaa ttgcagttcc	900
	ctggtggaac ccgtgggtgct ctgggtccgg gccaggtagt acagggtactg gtcgatgaga	960
	gggttcatca gccgggtctag gctctggctg tgcgcgtagc tgctgtggaa aggcacgtcc	1020
10	tcgaagctgt aactgaactc aaagtgtgtt cccgttctca gcatttgaga ggggaaatat	1080
	tccaggcagt agaaggagga acggcccacc gattggctgc cgttggtccag agtcaggtag	1140
	ccgtactgag gaatcatgaa gacgtccgcc gggaacggag gcaggcagcc ctggtgcgca	1200
15	gagccgagga cgtacggcag ctggtattcc gagtccgaga agacctgaac cgtgctggta	1260
	aggttatttag cgatgggtcgt gacgccgtca ttctgtgtga cctccttgac ctggatgttg	1320
	aggagcttga accgcagctt cttggggccgg aatccccagt tgttggtgat gagtcgctgc	1380
20	cagtcacgtg gtgagaagtg gcagtggaaat ctgttaaagt caaaataccc ccaggggggtg	1440
	ctgtagccga agtagtggtt gtcattgggtg gctcctgagc tgctgctgga gatttgcttg	1500
	tagaggtggt tgttgtaggt ggggagggcc caggttctgg tgctgggtggt gatgactctg	1560
25	tcgcccagcc atgtggaatc gcaatgccaa ttctctgagg cattaccac tccgtcggca	1620
	ccttcgttat tgtctgccat tgggtgcgcca ccgcctgcag ccattgtacc agatcccaca	1680
	ctagagggcg ctgctggagg ttctccaaga ggttgagggg cggggactga ctctgagtcg	1740
30	ccagtctgac caaaattgag cttcttttta gcgggctgct ggcctttttt gccgatgccc	1800
	gtggaggagt ctggagagcc tatgggtctc ttctttccag gagccgtctt agcgccttcc	1860
	tcaaccagac cgagaggttc gagaaccgcg ttcttggcct ggaagactgc tcgcccaggg	1920
35	ttgcccccaa atgacgtatc ttcttgacga cgctcctgaa actcggcgtc ggcgtgggta	1980
	taccgcaggt acggattgtc accgcctttg agctgctggt cgtaggcctt gtcgtgctcg	2040
	agggccgctg cgtccgccgc gttgacgggc tcccccttgt cgagtccgtt gaaggggtccg	2100
40	aggtacttgt agccaggaag caccagaccc cggccgtcgt cctgcttttg ctgggtggct	2160
	ttgggtttcg gggctccagg tttcaggtec caccactcgc gaatgccctc agagaggttg	2220
	tcctcgagcc aatctggaag ataaccatcg gcagccatac ctggtttaag tcatttattg	2280
45	ctcagaaaca cagtcgtcca ggtccacgtt gaccaggctc caggccgagc aagcaatctc	2340
	gggtgcccgc cccagcagat gatgaatcgc acacagcttc cgatacgtct ttttctgac	2400
	gaccgggtga gattctgaca cgccggggaa acattctaaa cagtctctga ccccgctcgt	2460
50	gaagcaaatg ttgaaattct gattcattct ctcgcacgtt ttgcagggaa acagcacctg	2520
	aagcatgccc gcgtgacgag aacatttggt ttggtacctg tcggcaaagt ccaccggagc	2580
	tccttccgcg tctgacgtcg atgggtccgt gactgagggg cgggcccgtt tgggtcgtc	2640
55	tatatccgcg tcatcggggg cgggtctttt gctggctccg ccctttctga cgtagaactc	2700

EP 1 310 571 B1

atgcgtcacc tcagtcacgt gatcactagc ccagcgggaag aactctttga cttcctgctt 2760
 5 tgtcaccttg ccaaagtcgt gttccagacg gcgggtgagt tcaaatttga acatccggtc 2820
 ctgcaacggt tgctggtgct cgaagggtggt gctgttcccg tcgatcacgg cgcacatggt 2880
 ggtgttgag gtgacgatca cgggggtggg atcgatctgg gcggacgact tgcacttttg 2940
 10 gtccacgcgc accttgctgc cgccgagaat ggccttggcg gactccacga ccttgggcgt 3000
 catcttgccc tcctcccacc agatcaccat cttgtcgacg caatcgttga agggaaagtt 3060
 ctcattggtc cagttgacgc agcaagggcg aattc 3095

15
 <210> 24
 <211> 3095
 <212> DNA
 <213> new AAV serotype, clone F5
 20
 <400> 24

25

30

35

40

45

50

55

EP 1 310 571 B1

	gaattcgccc	ttcgcagaga	ccaaagtcca	actgaaacga	atcaaccggg	ttattgatta	60
	acaagcaatt	acagattacg	ggtgaggtaa	cgagtgccaa	tggggcgagg	ctcagtataa	120
5	acaccatcag	ggttcacagc	aaattcaaca	ttattagact	tggcataatt	ggaagtatac	180
	tgaattttctg	ggttccagcg	cttgctgttt	tctttctgca	gctcccactc	gatttccacg	240
	ctgacttgtc	cggtgctgta	ctgcgtgatg	aaggaggcaa	acttggcagg	agtaaacacc	300
10	tccggaggat	tagcaggtag	aggtgtgttt	ttgatcagga	tctgtggagg	cgggtgttcg	360
	agtccaaaac	cgcccatcag	aggagacggg	tgaaagtgtc	catccgtgtg	aggaattttg	420
	gcccagatgg	gaccctgcag	atacacgtcc	cggttctgcc	agaccatgcc	aggcagtgtc	480
15	ccctggctgt	tgatagtctg	tgattgaggc	ccggctgtag	acgactgcag	gttgctggag	540
	accacaccgt	attcttctgt	agccacaggg	ttagtggtct	tgatctcttc	ctcgtctgtc	600
	atcagaacgt	tttccagcgt	agttttgttg	gcagctcccg	tcttgccaaa	aaccagtacc	660
20	ccgttgatgg	gaaagaactg	gtcctcatca	tccttggttg	ttgccatggg	aatgccagga	720
	ttggtcaaag	agtttctgcc	attcagatga	tatttagtgg	cagcagtcca	ggcaaaattg	780
	ctgttggtgt	taaagtccaa	gttctttgac	agtctctgtt	gcctatagca	gggtccaggc	840
25	agccagttct	ttgactgctc	ggccatagta	ttgggcccag	cttgatgaaa	ttgcagttcc	900
	ctggtggaac	ccgtggtgct	ctgggtccgg	gccaggtagt	acaggtagtg	gtcgatgaga	960
	gggttcatca	gccggtctag	gctctggctg	tgcgcgtagc	tgctgtggaa	aggcacgtcc	1020
30	tcgaagctgt	aactgaactc	aaagtgtgtg	cccgttctca	gcatttgaga	ggggaaatat	1080
	tccaggcagt	agaaggagga	acggcccacc	gattggctgc	cgttggttcag	agtcaggtag	1140
	ccgtactgag	gaatcatgaa	gacgtccgcc	gggaacggag	gcaggcagcc	ctggtgcgca	1200
35	gagccgagga	cgtacggcag	ctggtattcc	gagtccgaga	agacctgaac	cgtgctggta	1260
	aggttattag	cgatgggtcg	gacgccgtca	ttcgttggtg	cctccttgac	ctggatgttg	1320
40							
45							
50							
55							

EP 1 310 571 B1

aagagcttga accgcagctt cttggggccgg aatccccagt tgttggtgat gagtcgctgc 1380
 cagtcacgtg gtgagaagtg gcagtggaaat ctgttaaagt caaaataccc ccaggggggtg 1440
 5 ctgtagccga agtagtggtt gtcattggtg gctcctgagc tgctgctgga gatttgcttg 1500
 tagaggtggt tgttgtaggt ggggagggcc caggttctgg tgctggtggt gatgactctg 1560
 tcgcccagcc atgtggaatc gcaatgccaa tttcctgagg cattaccac tccgtcgga 1620
 10 ccttcgttat tgtctgccgt tgggtgcgca ccgcctgcag ccattgtacc agatcccaca 1680
 ctagagggcg ctgctggagg ttctccaaga ggttgagggg cggggactga ctctgagtcg 1740
 ccagtctgac caaaattgag cttcttttta gcgggctgct ggcctttttt gccgatgccc 1800
 15 gtggaggagt ctggagagtc tatgggtctc ttctttccag gagccgtctt agcgcccttc 1860
 tcaaccagac cgagaggttc gagaaccgc ttcttggcct ggaagactgc tcgcccaggg 1920
 ttgcccccaa atgacgtatc ttcttgagg cgctcctgaa actcggcgct gccgtggtta 1980
 20 taccgcaggt acggattgtc acccgctttg agctgctggt cgtaggcctt gtcgtgctcg 2040
 agggccgctg cgtccgccgc gttgacgggc tcccccttgt cgagtccgtt gaagggtccg 2100
 aggtacttgt agccaggaag caccagacc cggccgtcgt cctgcttttg ctggttggt 2160
 25 ttgggtttcg gggctccagg ttccaggtcc caccactcgc gaatgccctc agagaggttg 2220
 tcctcgagcc aatctggaag ataaccatcg gcagccatac ctggtttaag ccatttattg 2280
 ctcagaaaca cagtcgtcca ggtccacgtt gaccaggtcg caggccgagc aggcaatctc 2340
 30 gggtgcccgc ccagcagat gatgaatcgc acacagcttc cgatacgtct ttttctgac 2400
 gaccggttga gattctgaca cgccggggaa acattctaaa cagtctctga ccccgctcgt 2460
 gaagcaaattg ttgaaattct gattcattct ctgcacgtt ttgcaggga acagcatctg 2520
 35 aagcatgccc gcgtggcgag aacatttggt ttggtacctg tcggcaaagt ccaccggagc 2580
 tccttcgcgc tctgacgtcg atgggtccgt gactgagga caggcccgtc tgggctcgtc 2640
 tatatccgcg tcatcggggg cggtctttt gctggctccg ccctttctga cgtagaactc 2700
 40 atgcgtcacc tcagtcacgt gatcactagc ccagcggaag aactctttga cttcctgctt 2760
 tgtcacettg ccaaagtcgt gttccagacg gcgggtgagt tcaaatttga acatccggtc 2820
 ctgcaacggc tgctggtgct cgaagggtgt gctgttcccg tcgatcacgg cgcgcatgtt 2880
 45 ggtgttgag gtgacgatca cgggggtggg atcgatctgg gcggacgact tgacttttg 2940
 gtccacgcgc accttgctgc cgccgagaat ggccttggcg gactccacga ccttggccgt 3000
 catcttgccc tcctcccacc agatcaccat cttgtcgacg caatcggtga agggaaagt 3060
 50 ctcattggtc cagttgacgc agcaagggcg aattc 3095

<210> 25

<211> 3142

<212> DNA

<213> new AAV serotype, clone H6

EP 1 310 571 B1

<400> 25

	aaaacgacgg gccagtgatt gtaatacga cactatagg gcgaaattga aattagcggc	60
5	cgcgaattcg cctttcgcag agaccaaagt tcaactgaaa cgaattaaac ggtttattga	120
	ttaacaagca attacagatt acgagtcagg tatctggtgc caatggggcg aggctctgaa	180
	tacacaccat tagtgccac agtaaagtcc acattaacag acttggttga gttggaagtg	240
10	tactgaattt cgggattcca gcgtttgctg ttctccttct gcagctccca ctgatctcc	300
	acgctgacct gtcccgtgga atactgtgtg atgaaagaag caaacttggc agaactgaag	360
	tttgtgggag gattggctgg aacgggagtg tttttgatca tgatctgagg aggcgggtgt	420
15	ttgagtccaa aacctcccat cagtggagaa ggatgaaagt gtccatcggt gtgaggaatc	480
	ttggcccaa tgggtccctg caggtacacg tctcgatcct gccacacat accaggtaac	540
	gctccttggg gattgacagt tccagtagtt ggaccagtgt ttgagttttg caaattatct	600
20	gacacagtc cgtactgctc cgtagccacg ggattggtgg ccctgatttc ttcttcactc	660
	gtaatcatga catttttcaa atccgcgctg ttggcatttg ttccttgttt accaaatctc	720
	agggttccat gcatggggaa aaacttttct tcgtcatcct tgtgactggc catagctggg	780
25	cctggattaa ccaacgagtc cgggccattt agatgatact ttgtagctgc agtccaggga	840
	aagttgctgt tgttggtgtc gtttgccctgt ttgacagac gctgctgtct gtagcaaggt	900
	ccaggcagcc agtttttagc ttgaagagac atgttggttg gtccagcttg gctaaacagt	960
30	agccgagact gctgaagagt tccactatct gtttggtgtc tgttcagata atacaggtag	1020
	tggctgatca gaggattcat cagccgatcc agactctggc tgtgagcgtg gctgctgtgg	1080
	aaaggcacgt cttcaaaagt gtagctgaac tgaaagtgtt ttccagtacg cagcatctga	1140
35	gaaggaaagt actccaggca gtaaaaggaa gagcgtccta ccgcctgact cccgttgctc	1200
	agggtgaggt atccatactg tgggaccatg aagacgtccg ctggaaacgg cgggagggat	1260
	ccttgatgct ccgagcccag gacgtacggg agctggtact ccgagtcagt aaacacctga	1320
40	accgtgctgg taagggttatt ggcaatcgtc gtcgtaccgt cattctgctg gacctctttg	1380
	acttgaatat taaagagctt gaagttgagt cttttgggcc ggaatccccg gttgttgttg	1440
	acgagtcctt gccagtcacg tgggtgaaaag tggcagtgga atctgttgaa gtcaaaatac	1500
45	ccccaggggg tgctgtagcc aaagtagtgg ttgtcggtgc tggctcctga ttggctggag	1560
	atttgcttgt agaggtgggt gttgtatgtg ggcaggcccc aggttcgggt gctggtgggtg	1620
	atgactctgt cggccagcca ttgggaatcg caatgccaat ttcttgagga attaccact	1680
50	ccatcggcac cctcggttatt gtctgccatt ggtgcgccac tgcctgtagc cattgtagta	1740

55

EP 1 310 571 B1

gatcccagac cagagggggc tgctggtggc tgtccgagag gctggggggtc aggtacggag 1800
 tctgcgtctc cagtctgacc aaaatttaat ctttttcttg caggctgctg gcccgctttt 1860
 5 ccggttccccg aggaggagtc tggctccaca ggagagtgct ctaccggcct cttttttccc 1920
 ggagccgtct taacaggctc ctcaaccagg cccagagggt caagaaccct ctttttcgcc 1980
 tggaagactg ctctgcccag gttgccccca aaagacgtat cttctttaag gcgctcctga 2040
 10 aactctgcgt cggcgtggtt gtacttgagg tacgggttgt ctccgctgtc gagctgccgg 2100
 tcgtaggcct tgcgtgctc gagggccgcg gcgtctgcct cgttgaccgg ctcccccttg 2160
 tcgagtccgt tgaagggtcc gaggtacttg taccaggaa gcacaagacc cctgctgtcg 2220
 15 tccttatgcc gctctgcggg ctttggtggt ggtgggccag gtttgagctt ccaccactgt 2280
 cttattcctt cagagagagt gtccctcgagc caatctggaa gataaccatc ggcagccata 2340
 cctgatttaa atcatttatt gttcagagat gcagtcattc aaatccacat tgaccagatc 2400
 20 gcaggcagtg caagcgtctg gcacctttcc catgatatga tgaatgtagc acagtttctg 2460
 atacgccttt ttgacgacag aaacggggtg agattctgac acgggaaagc actctaaaca 2520
 gtctttctgt ccgtgagtga agcagatatt tgaattctga ttcattctct cgcattgtct 2580
 25 gcagggaac agcatcagat tcatgccac gtgacgagaa catttgtttt ggtacctgtc 2640
 cgcgtagtgt atcgaagctt ccgcgtctga cgtcgatggc tgcgcaactg actcgcgcgc 2700
 ccgtttgggc tcaattatat ctgcgtcact gggggcgggt cttttcttag ctccaccctt 2760
 30 tttgacgtag aattcatgct ccacctcaac cacgtgatcc tttgccacc ggaaaaagtc 2820
 tttcacttcc tgcttggtga cttttccaaa gtcattgatcc agacggcggg taagttcaaa 2880
 tttgaacatc cggctcttgca acggctgctg gtgctcgaag gtcgttgagt tcccgtcaat 2940
 35 cacggcgac atgttggtgt tggagggtgac gatcacggga gtcgggtcta tctgggccga 3000
 ggacttgcat ttctggtcca cagcacctt gcttcctcca agaattggctt tggccgactc 3060
 cagcaccttg gcggtcatct tcccctctc ccaccagatc accatcttgt cgacgcaatg 3120
 40 gtaaaaggaa agttctcatt gg 3142

<210> 26

<211> 3075

<212> DNA

<213> new AAV serotype, clone H2

<400> 26

50 tgagaacttt cttttcaacg attgcgtcgg acaagatggt gatctggtgg gaggagggga 60
 agatgaccgc caaggctcgt gagtcggcca aagccattct tggaggaagc aaggtgcgtg 120
 tggaccagaa atgcaagtcc tcggcccaga tagacccgac tcccgtgatc gtcacctcca 180
 55 acaccaacat gtgcgccgtg attgacggga actcaacgac cttcgagcac cagcagccgt 240
 tgcaagaccg gatgttcaaa tttgaactta cccgccgtct ggatcatgac tttggaaagg 300

EP 1 310 571 B1

	tcaccaagca ggaagtgaaa gactttttcc ggtgggcaaa ggatcacgtg gttgaggtgg	360
	agcatgaatt ctacgtcaaa aaggggtggag ctaagaaaag acccgcccc agtgacgcag	420
5	atataagtga gcccacacgg gcgcgcgagt cagttgcgca gccatcaacg tcagacgcgg	480
	aagcttcgat caactacgcg gacaggtacc aaaaacaaat gttctcgtca cgtgggcatg	540
	aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc	600
10	ttcactcacg gacagaaaga ctgttttagag tgctttcccg tgtcagaatc tcaaccogtt	660
	tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaaggtg	720
	ccagacgctt gcactgcctg cgatctggtc aatgtggatt tggatgactg catctctgaa	780
15	caataaatga tttaaatacag gtatggctgc cgatggttat cctccagatt ggctcgagga	840
	cactctctct gaagggataa gacagtgggtg gaagctcaaa cctggcccac caccaccaa	900
	gcccgcagag cggcataagg acgacagcag gggctctgtg cttcctgggt acaagtacct	960
20	cggacccttc aacggactcg acaaggggga gccggtcaac gaggcagacg ccgcggccct	1020
	cgagcacgac aaggcctacg accggcagct cgacagcgga gacaaccgt acctcaagta	1080
	caaccacgcc gacgcagagt ttcaggagcg ccttaaagaa gatacgtctt ttgggggcaa	1140
25	cctcggacga gcagtcttcc aggcgaaaaa gaggggttctt gaacctctgg gcctgggtga	1200
	ggaacctgtt aagacggctc cgggaaaaaa gaggccggta gagcactctc ctgtggagcc	1260
	agactcctcc tcgggaaccg gaaaagcggg ccagcggcct gcaagaaaaa gattaaattt	1320
30	tggtcagact ggagacgcag actccgtacc tgacccccag cctctcggac agccaccagc	1380
	agccccctct ggtctgggat ctactacaat ggctacaggc agtggcgcac caatggcaga	1440
	caataacgag ggtgccgatg gagtgggtaa ttcctcagga aattggcatt gcgattccca	1500
35	atggctgggc gacagagtca tcaccaccag caccgaacc tgggccctgc ccacatacaa	1560
	caaccacctc tacaagcaaa tctccagcca atcaggagcc agcaacgaca accactactt	1620
	tggtctacagc accccctggg ggtattttga cttcaacaga ttccactgcc acttttcacc	1680
40	acgtgactgg caaagactca tcaacaacaa ctggggattc cggcccaaaa gactcaactt	1740
	caagctcttt aatattcaag tcaaagaggt cagcgagaat gacggtagca cgacgattgc	1800
	caataacctt accagcacgg ttcaggtggt tactgactcg gaggaccagc tcccgtacgt	1860
45	cctgggctcg gcgcacaaag gatgcctccc gccgtttcca gcggacgtct tcatggctcc	1920
	acagtatgga tacctcacc tgaacaacgg gagtcaggcg gtaggacgct cttcctttta	1980
	ctgcctggag tactttcctt ctcagatgct gcgtactgga aacaactttc agttcagcta	2040
50	cacttttgaa gacgtgcctt tccacagcag ctacgctcac agccagagtc tggatcggct	2100
	gatgaatcct ctgatcgacc agtacctgta ttatctgaac aagacacaaa caaatagtgg	2160
55	aactcttcag cagtctcggc tactgttttag ccaagctgga ccaaccaaca tgtctcttca	2220

EP 1 310 571 B1

	agctaaaaac tggctgcctg gaccttgcta cagacagcag cgtctgtcaa aacaggcaaa	2280
	cgacaacaac aacagcaact ttccctggac tgcagctaca aagtatcatc taaatggccg	2340
5	ggactcgttg gttaatccag gaccagctat ggccagtcac aaggatgacg aagaaaagtt	2400
	tttccccatg catggaaccc tgatatttgg taaacaagga acaaatgcc aacgacgcgga	2460
	tttggaaaat gtcattgatta cagatgaaga agaaatcagg gccaccaatc ccgtgggtac	2520
10	ggagcagtac gggactgtgt caaataattt gcaaaactca aacactgggc caactactgg	2580
	aactgtcaat cgccaaggag cgttacctgg tatgggtgtg caggatcgag acgtgtacct	2640
	gcagggaccc atttgggcca agattcctca caccgatgga cactttcatc cttctccact	2700
15	gatgggaggt tttggactca aacacccgcc tcctcagatc atgatcaaaa acactcccgt	2760
	tccagccaat cctcccacaa acttcagttc tgccaagttt gcttctttca tcacacagta	2820
	ttccacggga caggtcagcg tggagatcga gtgggagctg cagaaggaga acagcaaacg	2880
20	ctggaatccc gaaattcagt acacttccaa ctacaacaag tctgttaatg tggactttac	2940
	tgtggacact aatggtgtgt attcagagcc tcgccccatt ggcaccagat acctgactcg	3000
	taatctgtaa ttgcttggtta atcaataaac cgtttaattc gtttcagttg aactttgggc	3060
25	tctgcgaagg gcgaa	3075

30	<210> 27
	<211> 3128
	<212> DNA
	<213> new AAV serotype, clone 42.8
35	<400> 27

40

45

50

55

EP 1 310 571 B1

	gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt	60
	gcgtcgacaa gatggtgatc tggtagggagg agggcaagat gacggccaag gtcgtggagt	120
5	ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaagtgc aagtcttccg	180
	cccagatcga tcccaccccc gtgatcgtca cttccaacac caacatgtgc gccgtgattg	240
	acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg	300
10	aactcaccgg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcaaagagt	360
	tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagtcttac gtcagaaagg	420
	gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct	480
15	gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg	540
	acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca	600
	agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact	660
20	gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc	720
	ggaaactctg tgccattcat catctgctag ggcgggctcc cgagattgct tgctcggcct	780
25		
30		
35		
40		
45		
50		
55		

EP 1 310 571 B1

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840
 ggtatggctg ccgatggtta tcttcagat tggctcgagg acaacctctc tgagggcatt 900
 5 cgcgagtggg gggacttgaa acctggagcc ccgaaacca aagccaacca gcaaagcag 960
 gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020
 gacaaggggg agcccgtaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080
 10 gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140
 tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcctc 1200
 caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260
 15 cctggaaaga agagaccggt agagccatca cccagcgtt ctccagactc ctctacgggc 1320
 atcggcaaga caggccagca gcccgcaaa aagagactca actttgggca gactggcgac 1380
 tcagagtcag tgcccgacce tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg 1440
 20 ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500
 gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560
 gtcatcacca ccagcaccgc aacctgggccc ctccccacct acaacaacca cctctacaag 1620
 25 caaatctcca acgggacatc gggaggaagc accaacgaca acacctactt cggtacagc 1680
 accccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740
 cagcgactca tcaacaacaa ctggggattc cggcccaaga gactcaactt caagctcttc 1800
 30 aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860
 accagcacga ttcaggctctt tacggactcg gaataccagc tcccgtacgt cctcggctct 1920
 gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980
 35 tacctgactc tgaacaacgg cagtcaggcc gtggggccgtt cctccttcta ctgcctggag 2040
 tactttcctt ctcaaatgct gagaacgggc aacaactttg agttcagcta ccagtttgag 2100
 gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gatgaacccc 2160
 40 ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga 2220
 actcagcagt tgctattttc tcaggccggg cctaataaca tgtcggctca ggccaaaaac 2280
 tggctaccgg ggccctgcta ccggcagcaa cgcgtctcca cgacactgtc gaaaaataac 2340
 45 aacagcaact ttgcttgga cgggtgccacc aagtatcatc tgaatggcag agactctctg 2400
 gtaaataccc gtgtcgctat ggcaacgcac aaggacgacg aagagcgatt ttttccatcc 2460
 agcggagtct tgatgtttgg gaaacaggga gctggaaaag acaacgtgga ctatagcagc 2520
 50 gttatgctaa ccagtgagga agaaatcaaa accaccaacc cagtggccac agaacagtac 2580
 ggcgtggtgg ccgataacct gcaacagcaa aacgccgctc ctattgtagg ggccgtcaac 2640
 agtcaaggag ccttacctgg catggtctgg cagaaccggg acgtgtacct gcagggtcct 2700
 55

EP 1 310 571 B1

	atctgggcca agattcctca cacggacggc aactttcatc cttcgccgct gatgggaggc	2760
	tttggactga aacacccgcc tcctcagatc ctgattaaga atacacctgt tcccgcggat	2820
5	cctccaacta ccttcagtca agccaagctg gcgtcgttca tcacgcagta cagcaccgga	2880
	caggtcagcg tggaaattga atgggagctg cagaaagaga acagcaagcg ctggaaccca	2940
	gagattcagt atacttccaa ctactacaaa tctacaaatg tggactttgc tgtcaatact	3000
10	gaggggtactt attcagagcc tcgccccatt ggcacccggt acctcacccg taacctgtaa	3060
	ttgcctgtta atcaataaac cggctaattc gtttcagttg aactttggtc tctgcgaagg	3120
	gcgaattc	3128

15

<210> 28

<211> 3128

<212> DNA

20

<213> new AAV serotype, clone 42.15

<400> 28

25

30

35

40

45

50

55

EP 1 310 571 B1

	gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt	60
	gcgtcgacaa gatggtgatc tgggtgggagg agggcaagat gacggccaag gtcgtggagt	120
5	ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg	180
	cccagatcga cccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg	240
	acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaaatttg	300
10	aactcaccgg ccgtctggag catgactttg gcaaggtgac aaagcaggaa gtcaaagagt	360
	tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg	420
	gtggagccaa caagagaccc gccccgatg acgcgataa aagcgagccc aagcgggcct	480
15	gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg	540
	acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca	600
	agacatgcga gagaatgaat cagaatttca acatttgctt cacgcgcggg accagagact	660
20	gttcagaatg tttcccgggc gtgtcagaat ctcaaccggc cgtcagaaag aggacgtatc	720
	ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct	780
	gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca	840
25	ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt	900
	cgcgagtggg gggacttgaa acctggagcc ccgaaacca aagccaacca gcaaaagcag	960
	gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc	1020
30	gacaaggggg agcccgtaa cgcggcggac gcagcggccc tcgagcacga caaggcctac	1080
	gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag	1140
	tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc	1200
35	caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct	1260

40

45

50

55

EP 1 310 571 B1

	cctggaaaga agagaccggt agagccatca cccagcggt ctccagactc ctctacgggc	1320
	atcggcaaga caggccagca gcccgcgaaa aagagactca actttgggca gactggcgac	1380
5	tcagagtcag tgcccgaacc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg	1440
	ggatctggta caatggctgc aggcgggtggc gctccaatgg cagacaataa cgaaggcgcc	1500
10	gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga	1560
	gtcatcacca ccagcaccgc aacctgggccc ctccccacct acaacaacca cctctacaag	1620
	caaatctcca acgggacatc gggagggaag accaacgaca acacctactt cggctacagc	1680
15	acccctctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg	1740
	cagcgactca tcaacaacaa ctgggggattc cggccaaga gactcaactt caagctcttc	1800
	aacatccagg tcaaggaggc cacgcagaat gaaggcacca agaccatcgc caataacctt	1860
20	accagcacga ttcagggtctt tacggactcg gaataccagc tcccgtagct cctcggtctt	1920
	gcgacaccagg gctgcccgc tccgttcccg gcggacgtct tcatgattcc tcagtacggg	1980
	tacctgactc tgaacaacgg cagtcaggcc gtgggcccgtt cctccttcta ctgcctggag	2040
25	tactttcctt ctcaaatgcg gagaacgggc aacaactttg agttcagcta ccagtttgag	2100
	gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gatgaacccc	2160
	ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga	2220
30	actcagcagt tgctattttc tcaggccggg cctaataaca tgtcggctca ggccaaaaac	2280
	tggctacccg ggccctgcta ccggcgagcaa cgcgtctcca cgacactgtc gcaaaataac	2340
	aacagcaact ttgcttggac cgggtgccacc aagtatcatc tgaatggcag agactctctg	2400
35	gtaaatcccg gtgtcgctat ggcaacgcac aaggacgacg aagagcgatt ttttccatcc	2460
	agcggagtct tgatgtttgg gaaacaggga gctggaaaag acaacgtgga ctatagcagc	2520
	gttatgctaa ccagttagga agaaatcaaa accaccaacc cagtggccac agaacagtac	2580
40	ggcgtggtgg ccgataacct gcaacagcaa aacgccgctc ctattgtagg ggccgtcaac	2640
	agtcaaggag ccttacctgg catgggtctgg cagaaccggg acgtgtacct gcagggtcct	2700
	atctgggcca agattcctca cacggacggc aactttcatc cttcgccgct gatgggaggc	2760
45	tttggactga aacaccgcgc tcctcagatc ctgattaaga atacacctgt tcccgcggat	2820
	cctccaacta ccttcagtca agccaagctg gcgtcgttca tcacgcagta cagcaccgga	2880
	caggtcagcg tggaaattga atgggagctg cagaaagaga acagcaagcg ctggaaccca	2940
50	gagattcagt atacttccaa ctactacaaa tctacaaatg tggactttgc tgtcaatact	3000
	gaggggtactt attcagagcc tcgccccatt ggcaccggtt acctacccg taacctgtaa	3060
	ttgcctgtta atcaataaac cggttaattc gtttcagttg aactttggtc tctgcgaagg	3120
55	gcgaattc	3128

<210> 29

EP 1 310 571 B1

<211> 3197

<212> DNA

<213> new AAV serotype. clone 42.5b

5

<400> 29

	gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt	60
10	gcgctcgacaa gatggtgatc tgggtgggagg agggcaagat gacggccaag gtcgtggagt	120
	ccgccaaggc cattctcggc ggcagcaagg tgcgctgga ccaaaagtgc aagtcgtccg	180
	cccagatcga cccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg	240
15	acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg	300
	aactcaccgg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcaaagagt	360
	tcttcgctg ggcgcaggat cacgtgaccg aggtggcgca tgagtcttac gtcagaaagg	420
20	gtggagccaa caagagaccc gccccgatg acgcggataa aagcgagccc aagcgggcct	480
	gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg	540
	acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca	600
25	agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact	660
	gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc	720
	ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct	780
30	gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca	840
	ggtatggctg ccgatggta tcttcagat tggctcgagg acaacctctc tgagggcatt	900
	cgcgagtggg gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag	960
35	gacgacggcc ggggtctggt gcttctctggc tacaagtacc tcggaccctt caacggactc	1020
	gacaagggag agccggtcaa cgaggcagac gccgcggccc tcgagcacga caaggcctac	1080
	gacaagcagc tcgagcaggg ggacaacccg tacctcaagt acaaccacgc cgacgccgag	1140
40	tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggag agcagtcttc	1200
	caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct	1260
	cctggaaaga agagaccggt agagccatca cccagcggt ctccagactc ctctacgggc	1320
45	atcggcaaga caggccagca gcccgcgaaa aagagactca actttgggca gactggcgac	1380
	tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg	1440
	ggatctggtg caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc	1500
50	gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga	1560
	gtcatcacca ccagcaccgg aacctgggccc ctccccacct acaacaacca cctctacaag	1620
	caaatctcca acgggacatc gggaggaagc accaaccgac acacctactt cggctacagc	1680
55	accccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg	1740

EP 1 310 571 B1

	cagcgactca tcaacaacaa ctggggattc cggcccaaga gactcaactt caagctcttc	1800
	aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt	1860
5	accagcacga ttcaggtctt tacggactcg gaataccagc tcccgtacgt cctcggctct	1920
	gcgacaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg	1980
	tacctgactc tgaacaacgg cagtcaggcc gtgggcccgtt cctccttcta ctgcctggag	2040
10	tacttttctt ctcaaagtct gagaacgggc aacaactttg agttcagcta ccagtttgag	2100
	gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gatgaacccc	2160
	ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga	2220
15	actcagcagt tgctatcttc tcaggccggg cctaataaca tgtcggctca ggccaaaaac	2280
	tggctacccg ggccctgcta ccggcagcaa cgcgtctcca cgacactgtc gcaaaataac	2340
	aacagcaact ttgcttggac cgggtgccacc aagtatcatc tgaatggcag agactctctg	2400
20	gtaaatcccg gtgtcgtat ggcaacgcac aaggacgacg aagagcgatt ttttccatcc	2460
	agcggagctt tgatgtttgg gaaacaggga gctggaaaag acaacgtgga ctatagcagc	2520
	gttatgctaa ccagttagga agaaatcaaa accaccaacc cagtggccac agaacagtac	2580
25	ggcgtggtgg ccgataacct gcaacagcaa aacgccgctc ctattgtagg ggccgtcaac	2640
	agtcaaggag ccttacctgg catggtctgg cagaaccggg acgtgtacct gcagggctct	2700
	atctgggcca agattcctca cacggacggc aactttcatc cttcgccgct gatgggaggc	2760
30	tttgactga aacacccgcc tcctcagatc ctgattaaga atacacctgt tcccgcggat	2820
	cctccaacta ctttcagtca agccaagctg gcgtcgttca tcacgcagta cagcaccgga	2880
	caggtcagcg tggaaattga atgggagctg cagaaagaga acagcaagcg ctggaaccca	2940
35	gagattcagt atacttccaa ctactacaaa tctacaaatg tggactttgc tgtcaatact	3000
	gagggacttt attcagagcc tcgccccatt ggcacccgtt acctcaccgg taacctgtaa	3060
	ttgcctgtta atcaataaac cggttaattc gtttcagttg aactttggtc tctgcgaagg	3120
40	gcgaattcgt ttaaacctgc aggactagtc ctttagtgga gggttaattc tgagcttggc	3180
	gtaatcatgg gtcatag	3197
45	<210> 30	
	<211> 2501	
	<212> DNA	
	<213> new AAV serotype, clone 42.1b	
50	<400> 30	
	gaattcgccc ttggctgctt caactggacc aatgagaact ttcccttcaa cgattgcgtc	60
	gacaagatgg tgatctggtg ggaggagggc aagatgacgg ccaaggctct ggagtccgcc	120
55	aaggccattc atcatctgct ggggccccgt cccgagattg cttgctcggc ctgcgatctg	180
	gtcaacgtgg acctggatga ctgtgtttct gagcaataaa tgacttaaac caggtatggc	240

EP 1 310 571 B1

	tgccgatggt tatcttccag attggctcga ggacaacctc tctgagggca ttcgcgagtg	300
	gtgggacttg agacctggag ccccgaaacc caaagccaac cagcaaaagc aggacgacgg	360
5	ccgggggtctg gtgcttctctg gctacaagta cctcggaccc ttcaacggac tcgacaaggg	420
	agagccgggtc aacgaggcag acgccgcggc cctcgagcac gacaaggcct acgacaagca	480
10	gctcgagcag ggggacaacc cgtacctcaa gtacaaccac gccgacgccg agtttcagga	540
	gcgtcttcaa gaagatacgt cttttggggg caacctcggg cgagcagtct tccaggccaa	600
	gaagcggggtt ctcgaacctc tcgggtctggt tgaggaaggc gctaagacgg ctcttgaaa	660
15	gaagagaccc atagaatccc ccgactcctc cacgggcatc ggcaagaaag gccagcagcc	720
	cgctaaaaag agactcaact ttgggcagac tggcgactca gagtcaagtgc ccgacctca	780
	accaatcgga gaaccccccg caggccccctc tgggtctggga tctggcacia tggctgcagg	840
20	cgggtggcgct ccaatggcag acaataacga aggcgccgac ggagtgggta gttcctcagg	900
	aaattggcat tgcgattcca catggctggg cgacagagtc atcaccacca gcacccgaac	960
	ctgggccctc cccacctaca acaaccacct ctacaagcaa atctccaacg ggacatcggg	1020
25	aggaagcacc aacgacaaca cctacttcgg ctacagcacc ccctgggggt attttgactt	1080
	taacagattc cactgccact tctcaccacg tgactggcag cgactcatca acaacaactg	1140
	gggattccgg cccaagagac tcaacttcaa gctcttcaac atccagggtca aggaggtcac	1200
30	gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc agcacgattc aggtctttac	1260
	ggactcggaa taccagctcc cgtacgtcct cggtctctgcg caccagggct gcctgcctcc	1320
	gttcccggcg gacgtcttca tgattcctca gtacgggtac ctgactctga acaacggcag	1380
35	tcaggccgtg ggccgttctt ccttctactg cctggagtac tttccttctc aaatgctgag	1440
	aacgggcaac aactttgagt tcagctacca gtttgaggac gtgccttttc acagcagcta	1500
	tgcgcacagc caaagcctgg accggctgat gaacccccctc atcgaccagt acctgtacta	1560
40	cctgtctcgg actcagtcca cgggagggtac cgcaggaact cagcagttgc tattttctca	1620
	ggccgggcct aataacatgt cggtcaggc caaaaactgg ctaccggggc cctgctaccg	1680
	gcagcaacgc gtctccacga cagtgtcgca aaataacaac agcaactttg cttggaccgg	1740
45	tgccaccaag tatcatctga atggcagaga ctctctggta aatcccgggtg tcgctatggc	1800
	aacgcacaag ggcgacgaag agcgattttt tccatccagc ggagtcttga tgtttgggaa	1860
	acagggagct ggaaaagaca acgtagacta tagcagcggt atgctaacca gtgaggaaga	1920
50	aatcaaaacc accaaccagc tggccacaga acagtacggc gtggtggccg ataacctgca	1980
	acagcaaaac gccgctccta ttgtaggggc cgtcaacagt caaggagcct tacctggcat	2040
	ggtctggcag aaccgggacg tgtacctgca gggtcctatc tgggccaaga ttectcacac	2100
55	ggacggcaac tttcatcctt cgccgctgat gggaggcttt ggactgaaac acccgctcc	2160

EP 1 310 571 B1

	tcagatcctg	attaagaata	cacctgttcc	cgcggatcct	ccaactacct	tcagtcaagc	2220
5	caagctggcg	tcgttcatca	cgcagtacag	caccggacag	gtcagcgtgg	aaattgaatg	2280
	ggagctgcag	aaagagaaca	gcaagcgctg	gaaccagag	attcagtata	cttccaacta	2340
	ctacaaatct	acaaatgtgg	actttgctgt	caatactgag	ggtacttatt	cagagcctcg	2400
10	ccccattggc	accggttacc	tcaccgtaa	cctgtaattg	cctgttaatc	aataaaccgg	2460
	ttgattcgtt	tcagttgaac	tttggctctc	agggcgaatt	c		2501

15	<210> 31
	<211> 3113
	<212> DNA
	<213> new AAV serotype, clone 42.13
20	<400> 31

25

30

35

40

45

50

55

EP 1 310 571 B1

	gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt	60
	gcgtcgacaa gatggtgata tgggtgggagg agggcaagat gacggccaag gtcgtggagt	120
5	ccgccaaggc cattctcggc ggcagcaagg tgcgctgga ccaaaagtgc aagtcgtccg	180
	cccagatcga tcccccccc gtgatcgta cttccaacac caacatgtgc gccgtgattg	240
	acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg	300
10	aactcaccgg ccgtctggag catgactttg gcaaggtgac aaagcaggaa gtcaaagagt	360
	tcttcgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg	420
	gtggagccaa caagagaccc gccccgatg acgcggataa aagcgagccc aagcgggcct	480
15	gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg	540
	acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca	600
	agacatgcga gagaatgaat cagaatttca acatttgctt cagcacggg accagagact	660
20	gttcagaatg tttccccggc gtgtcagaat ctcaaccggc cgtcagaaag aggacgtatc	720
	ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct	780
	gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca	840
25	ggtatggctg ccgatggtta tcttcagat tggctcgagg acaacctctc tgagggcatt	900
	cgcgagtggg gggacttgaa acctggagcc ccgaaacca aagccaacca gcaaaagcag	960
	gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc	1020
30	gacaaggggg agcccgtaa cgcggcggac gcagcggccc tcgagcacga caaggcctac	1080
	gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag	1140
	tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggag agcagtcttc	1200
35	caggccaaga agcgggttct cgaacctctc ggtctggtt aggaaggcgc taagacggct	1260
	cctggaaaga agagacccat agaatcccc gactcctcca cgggcatcgg caagaaaggc	1320
40	cagcagcccg ctaaaaagaa gctcaacttt gggcagactg gcgactcaga gtcagtgcc	1380
45		
50		
55		

EP 1 310 571 B1

5 gaccctcaac caatcggaga acccccgcga ggcccctctg gtctgggatc tgggtacaatg 1440
 gctgcaggcg gtggcgctcc aatggcagac aataacgaag gcgccgacgg agtgggtagt 1500
 tcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcac caccaccagc 1560
 acccgaacct gggccctccc cacctacaac aaccacctct acaagcaaatt ctccaacggg 1620
 10 acatcgggag gaagcaccaa cgacaacacc tacttcggct acagcacccc ctgggggtat 1680
 tttgacttta acagattcca ctgccacttc tcaccacgtg actggcagcg actcatcaac 1740
 aacaactggg gattccggcc caagagactc aacttcaagc tcttcaacat ccagggtcaag 1800
 gaggtcacgc agaataaagg caccaagacc atcgccaata accttaccag cagcattcag 1860
 15 gtcttttacgg actcgggaata ccagctcccg tacgtcctcg gctctgcgca ccagggtgc 1920
 ctgcctccgt tcccggcgga cgtcttcacg attcctcagt acgggtacct gactctgaac 1980
 aacggcagtc aggccgtggg ccgttcctcc ttctactgcc tggagtactt tccttctcaa 2040
 20 atgctgagaa cgggcaacaa ctttgagttc agctaccagt ttgaggacgt gccttttcac 2100
 agcagctatg cgcacagcca aagcctggac cggctgatga accccctcat cgaccagtac 2160
 ctgtactacc tgtctcggac tcagtcacg ggagggtaccg cagggaactca gcagttgcta 2220
 25 ttttctcagg ccgggcctaa taacatgtcg gctcaggcca aaaactggct acccgggccc 2280
 tgctaccggc agcaacgcgt ctccacgaca gtgtcgcaaa ataacaacag caactttgct 2340
 tggaccggtg ccaccaagta tcatctgaat ggcagagact ctctggtaaa tcccgggtgc 2400
 30 gctatggcaa cgcacaaggc cgacgaagag cgattttttc catccagcgg agtcttgatg 2460
 tttgggaaac agggagctgg aaaagacaac gtggactata gcagcgttat gctaaccagt 2520
 gaggaagaaa tcaaaaccac caaccagtg gccacagaac agtacggcgt ggtggccgat 2580
 35 aacctgcaac agcaaaacgc cgctcctatt gtaggggccg tcaacagtca aggagcctta 2640
 cctggcatgg tctggcagaa ccgggacgtg tacctgcagg gtcctatctg ggccaagatt 2700
 cctcacacgg acggcaactt tcatccttcg ccgctgatgg gagcctttgg actgaaacac 2760
 40 ccgcctcctc agatcctgat taagaataca cctgttcccg cggatcctcc aactaccttc 2820
 agtcaagcca agctggcgtc gttcatcacg cagtacagca ccggacaggc cagcgtggaa 2880
 attgaatggg agctgcagaa agagaacagc aagcgctgga acccagagat tcagtatact 2940
 45 tccaactact acaaactctac aaatgtggac tttgctgtca atactgaggg tacttattca 3000
 gagcctcgcc ccattggcac ccgttacctc acccgtagcc tgtaattgcc tgttaatcaa 3060
 50 taaaccgggt gattcgtttc agttgaactt tggctctctgc gaaggcgcaa ttc 3113

<210> 32

<211> 3113

<212> DNA

55 <213> new AAV serotype, clone 42.3a

<400> 32

EP 1 310 571 B1

	gaattcgccc	tttctacggc	tgcgtcaact	ggaccaatga	gaactttccc	ttcaacgatt	60
	gcgctcgacaa	gatggtgata	tgggtgggagg	agggcaagat	gacggccaag	gtcgtggagt	120
5	ccgccaaggc	cattctcggc	ggcagcaagg	tgcgcgtgga	ccaaaagtgc	aagtcgtccg	180
	cccagatcga	tcccaccccc	gtgatcgtca	cttccaacac	caacatgtgc	gccgtgattg	240
	acgggaaacag	caccaccttc	gagcaccagc	agccgttaca	agaccggatg	ttcaaatttg	300
10	aactcaccgg	ccgtctggag	catgactttg	gcaagggtgac	aaagcaggaa	gtcaaagagt	360
	tcttccgctg	ggcgcaggat	cacgtgaccg	aggtggcgca	tgagttctac	gtcagaaagg	420
	gtggagccaa	caagagaccc	gccccgatg	acgcggataa	aagcgagccc	aagcgggcct	480
15	gcccctcagt	cgcggtacca	tgcacgtcag	acgcggaagg	agctccggtg	gactttgccg	540
	acaggtacca	aaacaaatgt	tctcgtcacg	cgggcatgct	tcagatgctg	cttccctgca	600
	agacatgcga	gagaatgaat	cagaatttca	gcatttgctt	cacgcacggg	accagagact	660
20	gttcagaatg	tttccccggc	gtgtcagaat	ctcaaccggg	cgtcagaaaag	aggacgtatc	720
	ggaaactctg	tgccattcat	catctgctgg	ggcgggctcc	cgagattgct	tgctcggcct	780
	gcgatctggt	caacgtggac	ctggatgact	gtgtttctga	gcaataaatg	acttaaacca	840
25	ggtatggctg	ccgatggtca	tcttccagat	tggctcgagg	acaacctctc	tgagggcatt	900
	cgcgagtggg	gggacttgaa	acctggagcc	ccgaaaccca	aagccaacca	gcaaaaagcag	960
	gacgacggcc	ggggctctggt	gcttcctggc	tacaagtacc	tcggaccctt	caacggactc	1020
30	gacaaggggg	agcccgtcaa	cgcggcgagc	gcagcggccc	tcgagcacga	caaggcctac	1080
	gaccagcagc	tcaaagcggg	tgacaatccg	tacctgcggt	ataaccacgc	cgacgccgag	1140
	tttcaggagc	gtcttcaaga	agatacgtct	tttgggggca	acctcggggc	agcagtcttc	1200
35	caggccaaga	agcgggttct	cgaacctctc	ggtctggttg	aggaaggcgc	taagacggct	1260
	cctggaaaga	agagacccat	agaatcccc	gactcctcca	cgggcatcgg	caagaaaggc	1320
	cagcagcccc	ctaaaaagaa	gctcaacttt	gggcagactg	gcgactcaga	gtcagtcccc	1380
40	gacctcaac	caatcggaga	accccccgca	ggccccctct	gtctgggata	tgggtacaatg	1440
	gctgcaggcg	gtggcgctcc	aatggcagac	aataacgaag	gcgccgacgg	agtgggtagt	1500
	tcctcaggaa	attggcattg	cgattccaca	tagctggggc	acagagtcac	caccaccagc	1560
45	acccgaacct	gggccctccc	cacctacaac	aaccacctct	acaagcaaat	ctccaacggg	1620
	acatcggggag	gaagcaccaa	cgacaacacc	tacttcgggt	acagcacccc	ctgggggtat	1680
	tttgacttta	acagattcca	ctgccacttc	tcaccacgtg	actggcagcg	actcatcaac	1740
50	aacagctggg	gattccgggc	caagagactc	aacttcaagc	tcttcaacat	ccaggtcaag	1800
	gaggtcacgc	agaatgaagg	caccaagacc	atcgccaata	accttaccag	cacgattcag	1860
55	gtctttacgg	actcggaata	ccagctcccc	tacgtcctcg	gctctgcgca	ccagggctgc	1920

EP 1 310 571 B1

5
 10
 15
 20
 25
 30
 35

ctgcctccgt	tcccggcgga	cgtcttcatg	attcctcagt	acgggtacct	gactctgaac	1980
aacggcagtc	aggccgtggg	ccgttcctcc	ttctactgcc	tggagtactt	tcctttctcaa	2040
atgctgagaa	cgggcaacaa	ctttgagttc	agctaccagt	ttgaggacgt	gccttttcac	2100
agcagctacg	cgcacagcca	aagcctggac	cggctgatga	acccctcat	cgaccagtac	2160
ctgtactacc	tgtctcggac	tcagtccacg	ggagggtaccg	caggaactca	gcagttgcta	2220
ttttctcagg	ccgggcctaa	taacatgtcg	gctcaggcca	aaaactggct	acccggggccc	2280
tgtaccgggc	agcaacgcgt	ctccacgaca	ctgtcgcaaa	ataacaacag	caactttgct	2340
tggaccggtg	ccaccaagta	tcattctgaat	ggcagagact	ctctggtaaa	tcccgggtgtc	2400
gctatggcaa	cgcacaagga	cgcagaagag	cgattttttc	catccagcgg	agtcttgatg	2460
tttgggaaac	agggagctgg	aaaagacaac	gtggactata	gcagcgttat	gctaaccagt	2520
gaggaagaaa	tcaaaaccac	caaccagtg	gccacagAAC	agtacggcgt	ggtggccgat	2580
aacctgcaac	agcaaaacgc	cgctcctatt	gtaggggccc	tcaacagtca	aggagcctta	2640
cctggcatgg	tctggcagaa	ccgggacgtg	tacctgcagg	gtcctatctg	ggccaagatt	2700
cctcacacgg	acggcaactt	tcattccttcg	ccgctgatgg	gaggctttgg	actgaaacac	2760
ccgcctcctc	agatcctgat	taagaataca	cctgttcccg	cggatcctcc	aactaccttc	2820
agtcaagcca	agctggcgtc	gttcatcacg	cagtacagca	ccggacaggt	cagcgtggaa	2880
attgaatggg	agctgcagaa	agagaacagc	aagcgttggg	accagagat	tcagtatact	2940
tccaactact	acaaatctac	aaatgtggac	tttgctgtca	atactgaggg	tacttattca	3000
gagcctcgcc	ccattggcac	ccgttacctc	acccgtaacc	tgtaatgcc	tgttaatcaa	3060
taaaccggtt	aattcgtttc	agttgaactt	tggctctctgc	gaagggcgaa	ttc	3113

<210> 33

<211> 2504

<212> DNA

<213> new AAV serotype, clone 42.4

<400> 33

EP 1 310 571 B1

	gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt	60
	gcgtcgacaa gatggtgatc tgggtgggagg agggcaagat gacggccaag gtcgtggagt	120
5	ccgccaaggc cattcatcat ctgctggggc gggtctccga gattgcttgc tcggcctgcg	180
	atctggtcaa cgtggacctg gatgactgtg tttctgagca ataaatgact taaaccaggt	240
	atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc	300
10	gagtgggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac	360
	gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac	420
	aaggagagac cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac	480
15	aagcagctcg agcaggggga caaccctgac ctcaagtaca accacgccga cgccgagttt	540

20

25

30

35

40

45

50

55

EP 1 310 571 B1

	caggagcgtc ttcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag	600
	gccaagaagc gggttctcga acctctcggc ctggttgagg aaggcgctaa gacggctcct	660
5	ggaaagaaga gacccataga atccccgcac tcctccacgg gcatcggcaa gaaaggccag	720
	cagcccgccta aaaagaagct caacttttggg cagactggcg actcagagtc agtgcccgcac	780
	cctcaaccaa tcggagaacc ccccgagggc ccctctgggc tgggatcttg tacaatggct	840
10	gcaggcgggtg gcgctccaat ggcagacaat aacgaaggcg ccgacggagt gggtaatgcc	900
	tccggaaatt ggcattgcga ttccacatgg ctgggcgaca gagtcatcac caccagcacc	960
	cgcaacctggg ccctgcccac ctacaacaac cacctctaca agcagatata aagtcagagc	1020
15	ggggctacca acgacaacca cttcttcggc tacagcacc cctggggcta ttttgacttc	1080
	aacagattcc actgccactt ctcatcacgt gactggcagc gactcatcaa caacaactgg	1140
	ggattccggc ccaagagact caacttcaag ctcttcaaca tccaggtcaa ggaggtcacg	1200
20	cagaatgaag gcaccaagac catcgccaat aaccttacca gcacgattca ggtctttacg	1260
	gactcggaat accggctccc gtacgtcctc ggctctgcgc accagggctg cctgcctccg	1320
	ttcccggcgg acgtcttcat gattcctcag tacgggtacc tgactctgaa caacggcagt	1380
25	caggccgttg gccgttcctc cttctactgc ctggagtact ttccttctca aatgctgaga	1440
	acgggcaaca actttgagtt cagctaccag tttgaggacg tgccttttca cagcagctac	1500
	gcgcacagcc aaagcctgga ccggctgatg aacccctca tcgaccagta cctgtactac	1560
30	ctgtctcgga ctcagtcac gggaggtacc gcaggaactc agcagttgct attttctcag	1620
	gccgggccta ataacatgtc ggctcaggcc aaaaactggc taccggggcc ctgctaccgg	1680
	cagcaacgcg tctccacgac actgtcgcaa aataacaaca gcaactttgc ttggaccggt	1740
35	gccaccaagt atcatctgaa tggcagagac tctctggtaa atcccggtgt cgctatggca	1800
	acgcacaagg acgacgaaga gcgatttttt ccatccagcg gagtcttgat gtttgggaaa	1860
	caggagctg gaaaagacaa cgtggactat agcagcgta tgctaaccag tgaggaagaa	1920
40	atcaaaacca ccaaccagc ggccacagaa cagtacggcg tgggtggccga taacctgcaa	1980
	cagcaaaacg ccgctcctat tgtagggggc gtcaacagtc aaggagcctt acctggcatg	2040
	gtctggcaga accgggacgt gtacctgcag ggtcctatct gggccaagat tcctcacacg	2100
45	gacggcaact ttcatccttc gccgctgatg ggaggctttg gactgaaaca cccgcctcct	2160
	cagatcctga ttaagaatac acctgttccc gcggatcctc caactacctt cagtcaagcc	2220
	aagccggcgt cgttcatcac gcagtacagc accggacagg tcagcgtgga aattgaatgg	2280
50	gagctgcaga aagagaacag caagcgctgg aaccagaga ttcagtatac ttccaactac	2340
	tacaaatcta caaatgtgga ctttgctgtc aatactgagg gtacttatct agagcctcgc	2400
55	cccattggca cccgttacct caccgtaac ctgtaattgc ctgttaatca ataaaccggt	2460

EP 1 310 571 B1

taattcgttt cagttgaact ttggtctctg cgaagggcga attc

2504

5

<210> 34

<211> 3106

<212> DNA

<213> new AAV serotype, clone 42.5a

10

<400> 34

15

20

25

30

35

40

45

50

55

EP 1 310 571 B1

	gaattcgccc ttctacggct gcgtaactg gaccaatgag aactttccct tcaacgattg	60
	cgtcgacaag atggtgatct ggtgggagga gggcaagatg acggccaagg tcgtggagtc	120
5	cgccaaggcc attctcggcg gcagcaaggt gcgcgtggac caaaagtgc agtcgtccgc	180
	ccagatcgac cccacccccg tgatcgtcac ctccaacacc aacatgtgcg ccgtgattga	240
	cgggaacagc accaccttcg agcaccagca gccgttgacg gaccggatgt tcaaatttga	300
10	actcaccgc cgtctggagc atgacttttg caaggcgaca aagcaggaag tcaaagagtt	360
	cttcgcgtgg gcgcaggatc acgtgaccga ggtggcgcat gagttctacg tcagaaaggg	420
	tggagccaac aagagacccg ccccgatga cgcggaataa agcgagccca agcgggccccg	480
15	cccctcagtc gcggatccat cgacgtcaga cgcggaagga gctccggtgg actttgccga	540
	caggtaccaa aacaaatgtt ctctgtcacgc gggcatgctt cagatgctgt ttccctgcaa	600
	aacatgcgag agaatgaatc agaatttcaa catttgcttc acgcacggga ccagagactg	660
20	ttcagaatgt ttccccggcg tgtcagaatc tcaaccggtc gtcagaaaga ggacgtatcg	720
	gaaactctgt gccattcatc atctgtctggg gcgggctccc gagattgctt gctcggcctg	780
	cgatctggtc aacgtggacc tggatgactg tgtttctgag caataaatga cttaaaccag	840
25	gtatggctgc cgatggttat cttccagatt ggctcgagga caacctctct gagggcattc	900
	gcgagtgggtg ggacttgaaa cctggagccc cgaaacccaa agccaaccag caaaagcagg	960
	acgacggccg gggctctgggtg cttcctgggt acaagtacct cggacccttc aacggactcg	1020
30	acaagggaga gccggtcaac gaggcagacg ccgcggccct cgagcacgac aaggcctacg	1080
	acaagcagct cgagcagggg gacaaccctg acctcaagta caaccacgcc gacgccgagt	1140
	ttcaggagcg tcttcaagaa gatacgtctt ttgggggcaa cctcgggcca gcagtcttcc	1200
35	gggccaagaa gcgggttctc gaacctctcg gtctggttga ggaaggcgct aagacggctc	1260
	ctggaaagaa gagaccata gaatcccccg actcctccac gggcatcggc aagaaaggcc	1320
	agcagcccg ctaaaaagaag ctcaactttg ggcagactgg cgactcagag tcagtccccg	1380
40	accccccaacc tctcggagaa cctcccgcg cgccctcagg tctgggatct ggtacaatgg	1440
	ctgcaggcgg tggcgacca atggcagaca ataacgaagg cgccgacgga gtgggtaatg	1500
	cctccggaat ttggcattgc gattccacat ggctgggcca cagagtcac accaccagca	1560
45	cccgcacctg ggccctgcc acctacaaca accacctcta caagcagata tcaagtcaga	1620
	gcggggctac caacgacaac cacttcttcg gctacagcac ccctggggc tattttgact	1680

50

55

EP 1 310 571 B1

	tcaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatc aacaacaacc	1740
	ggggattccg gcccagaaag ctgcggttca agttgttcaa catccaggtc aaggagggtca	1800
5	cgacgaacga cggcggttacg accatcgcta ataaccttac cagcacgatt caggtcttct	1860
	cggactcgga gtaccaactg ccgtagctcc tcggctctgc gcaccagggc tgcctccctc	1920
10	cgttccctgc ggacgtgttc atgattcctc agtacggata tctgactcta aacaacggca	1980
	gtcagtcgtgt gggacgttcc tccttctact gcctggagta ctttccttct cagatgctga	2040
	gaacgggcaa taactttgaa ttcagctacc agtttgagga cgtgcccttt cacagcagct	2100
15	acgcgcacag ccaaagcctg gaccggctga tgaacccct catcgaccag tacctgtact	2160
	acctgtctcg gactcagtc cggggaggta ccgcaggaac tcagcagttg ctattttctc	2220
	aggccggggc taataacatg tcggctcagg ccaaaaactg gctaccggg ccctgctacc	2280
20	ggcagcaacg cgtctccacg aactgtcgc aaaataacaa cagcaacttt gcttgaccg	2340
	gtgccaccaaa gtatcatctg aatggcagag actctctggt aaatcccggt gtcgctatgg	2400
	caacgcacaa ggacgacgaa gagcgatttt ttccatccag cggagtcttg atgtttggga	2460
25	aacagggagc tggaaaagac aacgtggact atagcagcgt tatgctaacc agtgaggaag	2520
	aaatcaaaac caccaaccca gtggccacag aacagtacgg cgtggtggcc gataacctgc	2580
	aacagcaaaa cgccgctcct attgtagggg ccgtcaacag tcaaggagcc ttacctggca	2640
30	tggcctggca gaaccgggac gtgtacctgc agggtcctat ctgggccaag attcctcaca	2700
	cggacggcaa ctttcatcct tcgccgctga tgggaggctt tggactgaaa caccgcctc	2760
	ctcagatcct gattaagaat acacctgttc ccgcggatcc tccaactacc ttcagtcaag	2820
35	ccaagctggc gtcgttcac acgcagtaca gcaccggaca ggtcagcgtg gaaattgaat	2880
	gggagctgca gaaagagaac agcaagcgtt ggaaccacaga gattcagtat acttccaact	2940
	actacaaatc tacaaatgtg gactttgctg tcaatactga gggtaacttat tcagagcctc	3000
40	gccccattgg cacccggtac ctcaccgta acctgtaatt gcctgttaat caataaacgg	3060
	gttaattcgt ttcagttgaa ctttggcttc tgcgaagggc gaattc	3106

<210> 35

<211> 2489

<212> DNA

<213> new AAV serotype, clone 42.10

<400> 35

EP 1 310 571 B1

	gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt	60
	gcgtcgacaa gatggtgatc tgggtgggagg agggcaagat gacggccaag gtcgtgaagt	120
5	ccgccaaggc cattcatcat ctgctggggc gggctcccga gattgcttgc tcggcctgcg	180
	atctggtcaa cgtggacctg gatgactgtg tttctgagca ataaatgact taaaccaggt	240
	atggctgccg atgggttatct tccagattgg ctgaggaca acctctctga gggcattcgc	300
10		
15		
20		
25		
30		
35		
40		
45		
50		
55		

EP 1 310 571 B1

gagtgggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 360
 gacggccggg gtctggtgct tcttggttac aagtacctcg gacccttcaa cggactcgac 420
 5 aagggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 480
 aagcagctcg agcaggggga caaccgtac ctcaagtaca accacgccga cggcaggttt 540
 caggagcgtc ttcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 600
 10 gccaaagaagc ggggttctcga acctctcggg ctgggttgagg aaggcgctaa gacggctcct 660
 ggaaagaaga gacccataga atcccccgac tcctccacgg gcatcggcag gaaaggccag 720
 cagcccgcta aaaagaagct caactttggg cagactggcg actcagagtc agtgcccgac 780
 15 cctcaaccaa tcggagaacc ccccgaggc ccctctggtc tgggatctgg tacaatggct 840
 gcaggcgggtg gcgctccaat ggcagacaat aacgaaggcg ccgacggagt gggtaatgcc 900
 tccggaaatt ggcatctcga ttccacatgg ctgggcgaca gagtcatcac caccagcacc 960
 20 cgcacctggg ccctgcccac ctacaacaac cacctctaca agcagatata aagtcagagc 1020
 ggggctacca acgacaacca cttcttcggc tacagcacc cctggggcta ttttgacttc 1080
 aacagattcc actgccactt ctcaccacgt gactggcagc gactcatcaa caacaactgg 1140
 25 ggattccggc ccagaaagct gcgggtcaag ttgttcaaca tccagggtcaa ggaggtcacg 1200
 acgaacgacg gcgttacgac catcgccaat aaccttacca gcacgattca ggtcttctcg 1260
 gactcggagt accaactgcc gtacgtcctc ggctctgcgc accagggtcg cctccctccg 1320
 30 ttccctgcgg acgtgttcat gattcctcag tacggatata tgactctaaa caacggcagt 1380
 cagtctgtgg gacgttcctc cttctactgc ctggagtact ttcttctca gatgctgaga 1440
 acgggcaata actttgaatt cagctacacc tttgaggaag tgcctttcca cagcagctat 1500
 35 gcgcacagcc agagcctgga ccggctgatg aatccctca tcgaccagta cctgtactac 1560
 ctggcccggg cccagagcac tacggggtcc acaagggagc tgcagttcca tcaggctggg 1620
 cccaacacca tggccgagca atcaaagaac tggctgcccg gaccctgtta tcggcagcag 1680
 40 agactgtcaa aaaacataga cagcaacaac aacagtaact ttgcctggac cggggccact 1740
 aaataccatc tgaatggtag aaattcatta accaaccgg gcgtagccat ggccaccaac 1800
 aaggacgacg aggaccagt ctttcccatc aacggagtgc tggtttttgg caaacgggg 1860
 45 gctgccaaca agacaacgct ggaaaacgtg ctaatgacca gcgaggagga gatcaaaacc 1920
 accaatcccg tggctacaga agaatacggg gtggctctcca gcaacctgca atcgtctacg 1980
 gccggacccc agacacagac tgtcaacagc cagggggctc tgcccggcat ggtctggcag 2040
 50 aaccgggacg tgtacctgca ggggtccatc tgggccaaaa ttctcacac ggacggcaac 2100
 tttcacccgt ctcccctgat gggcggtttt ggaactcaaac acccgctcc tcaaattctc 2160
 atcaaaaaca ccccggtacc tgctaatcct ccagagggtg ttactcctgc caagtttgcc 2220
 55

EP 1 310 571 B1

tcatttatca cgcagtacag caccggccag gtcagcgtgg agatcgagtg ggaactgcag 2280
 aaagaaaaca gcaaacgctg gaatccagag attcagtaca cctcaaatta tgccaagtct 2340
 5 aataatgtgg aatttgctgt caacaacgaa ggggtttata ctgagcctcg ccccatggc 2400
 acccgttacc tcaccgtaa cctgtaattg cctgttaatc aataaaccgg ttaattcggt 2460
 tcagttgaac tttggtcaag ggcgaattc 2489

10

<210> 36

<211> 2495

<212> DNA

15

<213> new AAV serotype, clone 42.3b

<400> 36

20

25

30

35

40

45

50

55

EP 1 310 571 B1

	gaattcgccc	tttctacggc	tgcgtcaact	agaccaatga	gaactttccc	ttcaacgatt	60
	gcgtcgacaa	gatggtgatc	tgggtgggagg	agggcaagat	gacggccaag	gtcgtggagt	120
5	ccgccaaggc	cattcatcat	ctgctggggc	gggctcccga	gattgcttgc	tcggcctgcg	180
	atctggtcaa	cgtggacctg	gatgactgtg	tttctgagca	ataaatgact	taaaccaggt	240
	atggctgccc	atggttatct	tccagattgg	ctcgaggaca	acctctctga	gggcattcgc	300
10	gagtgggtggg	acttgaaacc	tggagccccg	aaacccaaag	ccaaccagca	aaagcaggac	360
	gacggccggg	gtctgggtgct	tcctgggtac	aagtacctcg	gacccttcaa	cggactcgac	420
	aagggagagc	cgggtcaacga	ggcagacgcc	gcggccctcg	agcacgacaa	ggcctacgac	480
15	aagcagctcg	agcaggggga	caacccttac	ctcaagtaca	accacgccga	cggcaggttt	540
	caggagcgtc	ttcaagaaga	tacgtctttt	gggggcaacc	tcgggcgagc	agtcttccag	600
	gccaagaagc	gggttctcga	acctctcggg	ctggttgagg	aaggcgctaa	gacggctcct	660
20	ggaaagaaga	gacccataga	atcccccgac	tcctccacgg	gcatcggcaa	gaaaggccag	720
	cagcccgcta	aaaagaagct	caactttggg	cagactggcg	actcagagtc	agtgcccgac	780
	cctcaaccaa	tcgggagaacc	ccccgcaggc	ccctctggtc	tgggatctgg	tacaatggct	840
25	gcaggcggtg	gcgctccaat	ggcagacaat	aacgaaggcg	ccgacggagt	gggtaatgcc	900
	tccggaaatt	ggcattgcga	ttccacatgg	ctgggcgaca	gagtcatcac	caccagcacc	960
	cgcacctggg	ccctgcccac	ctacaacaac	cacctctaca	agcagatata	aagtcagagc	1020
30	ggggctacca	acgacaacca	cttcttcggc	tacagcacc	cctgggggcta	ttttgacttc	1080
	aacagattcc	actgccactt	ctcaccacgt	gactggcagc	gactcatcaa	caacaactgg	1140
	ggattccggc	ccagaaagct	gcggttcaag	ttgttcaaca	tccagggtcaa	ggaggtcacg	1200
35	acgaacgacg	gcgttacgac	catcgctaata	aaccttacca	gcacgattca	ggtcttctcg	1260
	gactcggagt	accaactgcc	gtacgtcctc	ggctctgcgc	accagggtcg	cctccctccg	1320
	ttccctgcgg	acgtgttcat	gattcctcag	tacggatatc	tgactctaaa	caacggcagt	1380
40	cagtctgtgg	gacgttcctc	cttctactgc	ctggagtact	ttccttctca	gatgctgaga	1440

45

50

55

EP 1 310 571 B1

	acgggcaata actttgaatt cagctacacc tttgaggaag tgcctttcca cagcagctat	1500
	gcgcacagcc agagcctgga ccggctgatg aatccctca tcgaccagta cctgtactac	1560
5	ctggcccga cccagagcac tacggggtcc acaagggagc tgcagttcca tcaggctggg	1620
	cccaacacca tggccgagca atcaaagaac tggctgccc gacctgtta tcggcagcag	1680
	agactgtcaa aaaacataga cagcaacaac accagtaact ttgcctggac cggggccact	1740
10	aaataccatc tgaatggtag aaattcatta accaaccgg gcgtagccat ggccaccaac	1800
	aaggacgacg aggaccagtt ctttcccatc aacggagtg tggtttttg caaaacgggg	1860
	gctgccaaac agacaacgct ggaaaacgtg ctaatgacca gcgaggagga gatcaaaacc	1920
15	accaatcccg tggctacaga acagtacggt gtggtctcca gcaacctgca atcgtctacg	1980
	gccggacccc agacacagac tgtcaacagc cagggggctc tgcccggcat ggtctggcag	2040
	aaccgggacg tgtacctgca ggggtccatc tgggccaaaa ttcctcacac ggacggcaac	2100
20	tttcaccgct ctcccctgat gggcggtatt ggactcaaac accgcctcc tcaaattctc	2160
	atcaaaaaca ccccggtacc tgctaatact ccagaggtgt ttactcctgc caagtttgcc	2220
	tcatttatca cgcagtacag caccggccag gtcagcgtgg agatcgagtg ggaactgcag	2280
25	aaagaaaaca gcaaacgctg gaatccagag attcagtaca cctcaaatta tgccaagtct	2340
	aataatgtgg aatttgctgt caacaacgaa ggggtttata ctgagcctcg cccattggc	2400
	accggttacc tcaccgtaa cctgtaattg cctgttaatc aataaaccgg ttaattcgtt	2460
30	tcagttgaac tttggtctct gcgaaggcg aatc	2495

<210> 37

<211> 3098

35 <212> DNA

<213> new AAV serotype, clone 42.11

<400> 37

40	gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt	60
	gcgtcgacaa gatggtgatc tgggtgggagg agggcaagat gacggccaag gtcgtggagt	120
	ccgccaaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcttccg	180
45	cccagatcga tcccaccccc gtgatcgtca cttccaacac caacatgtgc gccgtgattg	240
	acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg	300
	aactcaccg ccgtctggag cacgactttg gcaagggtgac aaagcaggaa gtcaaagagt	360
50	tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg	420
	gtggagccaa caagagaccc gccccgatg acgcggataa aagcgagccc aagcgggcct	480
	gcccctcagt cgcggtacca tcgacgtcag acgcggaagg agctccggtg gactttgccg	540
55	acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca	600
	agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accggagact	660

EP 1 310 571 B1

	gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaaag aggacgtatc	720
	ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct	780
5	gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca	840
	ggtatggctg ccgatggtta tcttcagat tggctcgagg acaacctctc tgagggcatt	900
	cgcgagtggg gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag	960
10	gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc	1020
	gacaagggag agccgggtcaa cgcgggcgac gcagcggccc tcgagcacga caaggcctac	1080
	gaccagcagc tcaaagcggg tgacaatccg tacctgcggg ataaccacgc cgacgccgag	1140
15	tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc	1200
	caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggtc	1260
	cctggaaaga agagacctat agaatcccc gactcctcca cgggcatcgg caagaaaggc	1320
20	cagcagcccg ctaaaaagaa gctcaacttt gggcagactg gcgactcaga gtcagtgcc	1380
	gacctcaac caatcggaga acccccgcga ggcccctctg gtctgggatc tgggtacaatg	1440
	gctgcaggcg gtggcgctcc aatggcagac aataacgaag gcgccgacgg agtgggtaat	1500
25	gcctccggaa attggcattg cgattccaca tggctgggcg acagagtcac caccaccagc	1560
	accgcacct gggccctgcc cacctacaac aaccacctct acaagcagat atcaagtcag	1620
	agcggggcta ccaacgacaa ccacttcttc ggctacagca cccctgggg ctattttgac	1680
30	ttcaacagat tccactgcc cttctcacca cgtgactggc agcgactcat caacaacaac	1740
	tggggattcc ggcccagaaa gctgcgggtc aagtgtttca acatccaggt caaggaggtc	1800
	acgacgaacg acggcggttac gaccatcgct aataacctta ccagcacgat tcagggtcttc	1860
35	tcggactcgg agtaccact gccgtacgtc ctgggctctg cgcaccaggg ctgcctccct	1920
	ccgttccttg cggacgtggt catgattcct cagtacggat atctgactct aaacaacggc	1980
	agtcagtctg tgggacgttc ctctttctac tgcttgaggt actttccttc tcagatgctg	2040
40	agaacgggca ataactttga attcagctac acctttgagg aagtgccttt ccacagcagc	2100
	tatgcgcaca gccagagcct ggaccggctg atgaatcccc tcatcgacca gtacctgtac	2160
	tacctggccc ggaccagag cactacgggg tccacaaggg agctgcagtt ccatcaggct	2220
45	gggcccacaa ccatggccga gcaatcaaag aactggctgc ccggaccctg ttatcggcgg	2280
	cagagactgt caaaagacat agacagcaac aacaacagta actttgcctg gaccggggcc	2340
	actaaatacc atctgaatgg tagaaattca ttaaccaacc cgggcgtagc catggccacc	2400
50	aacaaggacg acgaggacca gttctttccc atcaacggag tgctggtttt tggcaaacg	2460
	ggggctgcc acaagacaac gctggaaaac gtgctaataa ccagcgagga ggagatcaaa	2520
55	accaccaate ccgtggctac agaagaatac ggtgtggtct ccagcaacct gcaatcgtct	2580

EP 1 310 571 B1

	acggccggac cccagacaca gactgtcaac agccaggggg ctctgcccgg catggtctgg	2640
	cagaaccggg acgtgtacct gcaggggtccc atctgggccca aaattcctca cacggacggc	2700
5	aactttcacc cgtctcccct gatgggcgga ttggactca aacacccgcc tcctcaaatt	2760
	ctcatcaaaa acaccccggg acctgctaata cctccagagg tgtttactcc tgccaagttt	2820
	gcctcattta tcacgcagta cagcaccggc caggtcagcg tggagatcga gtgggaactg	2880
10	cagaaagaga acagcaaacg ctggaatcca gagattcagt acacctcaaa ttatgccaag	2940
	tctaataatg tggaatttgc tgtcaacaac gaaggggttt atactgagcc tcgccccatt	3000
	ggcaccgggt acctcaccgg taacctgtaa ttacttggtta atcaataaac cgggttgattc	3060
15	gtttcagttg aactttgggc tctgcgaagg gcgaattc	3098

20	<210> 38
	<211> 3276
	<212> DNA
	<213> new AAV serotype, clone 42.6a
25	<400> 38

30

35

40

45

50

55

EP 1 310 571 B1

	gaattcgccc	ttcgagaga	ccaaagttca	actgaaacga	attaaccggt	ttattgatta	60
	acaggcaatt	acaggttacg	ggtgaggtaa	cgggtgccaa	tggggcgagg	ctcagtataa	120
5	accccttcgt	tgttgacagc	aaattccaca	ttattagact	tggcataatt	tgagggtgtac	180
	tgaatctctg	gattccagcg	tttgctgttt	tctttctgca	gttcccaactc	gatctccacg	240
	ctgacctggc	cggctgtgta	ctgctgtgata	aatgaggcaa	acttggcagg	agtaaaccacc	300
10	tctggaggat	tagcaggtag	cggggtgttt	ttgatgagaa	tttgaggagg	cgggtgtttg	360
	agtccaaatc	cgtccatcag	gggagacggg	tgaaagttgc	cgtccgtgtg	aggaattttg	420
	gccagatgg	gacctgcag	gtacacgtcc	cggttctgcc	agaccatgcc	gggcagagcc	480
15	ccctggctgt	tgacagtctg	tgtctggggg	ccggccgtag	acgattgcag	gttctctggag	540
	accacacogt	attcttctgt	agccacggga	ttggtgtgtt	tgatctcctc	ctcgtctggtc	600
	attagcacgt	tttccagcgt	tgtcttgttg	gcagcccccg	ttttgccaaa	aaccagcact	660
20	ccgttgatgg	gaaagaactg	gtcctcgctg	tccttggttg	tggccatggc	tacgcccggg	720
	ttggttaatg	aatttctacc	attcagatgg	tatttagtgg	ccccggtcca	ggcaaagtta	780
	ctgttggtgt	tgctgtctat	gttttttgac	agtctctgct	gccgataaca	gggtccgggc	840
25	agccagttct	ttgattgctc	ggccatgggt	ttggggccag	cctgatggaa	ctgcagctcc	900
	cttgtggacc	ccgtagtgtc	ctgggtccgg	gccaggtagt	acaggtagct	gtcgatgagg	960
	ggattcatca	gccgggtccag	gctctggcta	tgcgcatagc	tgctgtggaa	aggcacttcc	1020
30	tcaaagggtg	agctgaattc	aaagttattg	cccgttctca	gcattctgaga	aggaaagtac	1080
	tccaggcagt	agaaggagga	acgtccacac	gactgactgc	cgttgtttag	agtcagatat	1140
35	ccgtactgag	gaatcatgaa	cacgtccgca	gggaacggag	ggaggcagcc	ctggtgcgca	1200
40							
45							
50							
55							

EP 1 310 571 B1

	gagccgagga cgtacggcag ttggtactcc gagtccgaga agacctgaat cgtgctggta	1260
	aggttattag cgatgggtcgt aacgccgtcg tccgtcgtga cctccttgac ctggatgttg	1320
5	aacaacttga accgcagctt tctgggccgg aatccccagt tgttggtgat gagtcgctgc	1380
	cagtcacgtg gtgagaagtg gcagtggaaat ctgttaaagt caaaataccc ccaggggggtg	1440
10	ctgtagccga agtaggtgtt gtcgttggtg cttcctcccg atgtcccgtt ggagatttgc	1500
	ttgtagaggt ggttggtgta ggtggggagg gcccaggttc ggggtgctggt ggtgatgact	1560
	ctgtcgccca gccatgtgga atcgcaatgc caatttcctg aggaactacc cactccgtcg	1620
15	gcgccttcgt tattgtctgc cattggagcg ccaccgcctg cagccattgt accagatccc	1680
	agaccagagg ggcctgcggg gggttctccg attggttag ggtcgggcac tgactctgag	1740
	tcgccagtct gcccaaagtt gagtctcttt ttcgcgggct gctggcctgt cttgccgatg	1800
20	cccgtagagg agtctggaga acgctggggg gatggctcta ccggtctctt ctttccagga	1860
	gccgtcttag cgcttcctc aaccagaccg agaggttcga gaaccgcctt cttggcctgg	1920
	aagactgctc gcccgagggt gcccccacaa gacgtatctt cttgaagacg ctctgaaac	1980
25	tcggcgctcg cgtgggtgta cttgaggtag gggttgtccc cctgctcgag ctgcttgctg	2040
	taggccttgt cgtgctcgag ggcgcggcg tctgcctcgt tgaccggctc tcccttgctg	2100
	agtccttga aggggtccgag gtactttag ccaggaagca ccagaccccg gccgtcgctc	2160
30	tgcttttgct ggttggtctt gggtttcggg gctccagggt tcaagtccca cactcgcga	2220
	atgccctcag agaggttgtc ctcgagccaa tctggaagat aaccatcggc agccatacct	2280
	ggtttaagtc atttattgct cagaaacaca gtcacccagg tccacgttga ccagatcgca	2340
35	ggccgagcaa gcaatctcgg gagcccgcc cagcagatga tgaatggcac agagtttccg	2400
	atacgtcctc tttctgacga ccggttgaga ttctgacacg ccggggaaac attctgaaca	2460
	gtctctggtc ccgtgcgtga agcaaatgtt gaaattctga ttcattctct cgcatgtctt	2520
40	gcagggaaac agcatctgaa gcatgccgc gtgacgagaa cacttgtttt ggtacctgtc	2580
	ggcaaagtcc accggagctc cttccgcgtc tgacgtcgat ggatgcaaaa tgtcgcaaaa	2640
	gcactcacgt gacagctaata acaggaccac tcccctatga cgtgatttac gtcagcgcta	2700
45	tgcccgctg acgagaacat ttgttttggt acctgtcggc aaagtccacc ggagctcctt	2760
	ccgcgtctga cgtcgatgga tccgcgactg aggggcaggc ccgcttgggc tcgcttttat	2820
	ccgcgtcctc gggggcggtt ctcttggttg ctcaccctt tctgacgtag aactcatgcg	2880
50	ccacctcggt cagtgatcc tgcgcccagc ggaagaactc tttgacttcc tgctttgtca	2940
	ccttgccaaa gtcatgctcc agacggcggg tgagttcaaa tttgaacatc cggctctgca	3000
	acggctgctg gtgctcgaag gtggtgctgt tcccgctcaat cacggcgcac atgttggtgt	3060
55	tggaagtgac gatcacgggg gtgggatcga tctgggcgga agacttgac ttttggtcca	3120

EP 1 310 571 B1

```

cgcgcacctt gctgccgccg agaatggcct tggcggactc cagcaccttg gccgtcatct 3180
tgcectcctc ccaccagatc accatcttgt cgacgcaatc gttgaaggga aagttctcat 3240
5   tgggccagtt gacgcagccg tagaaagggc gaattc 3276

```

<210> 39

<211> 3084

<212> DNA

<213> new AAV serotype, clone 43.1

<400> 39

EP 1 310 571 B1

	gaattcgccc tttctacggc tgcatacaact ggaccaatga gaactttccc ttcaacgatt	60
	gcgtcgacaa gatggtgatc tggtagggagg agggcaagat gacggccaag gtcgtggagt	120
5	ccgccaaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg	180
	cccagatcga cccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg	240
	acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaagttcg	300
10	aactcaccgg ccgtctggag cacgactttg gcaagggtgac caagcaggaa gtcaaagagt	360
	tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg	420
	gcgggagccag caaaagaccc gcccccgatg acgcggatat aagcgagccc aagcgggcct	480
15	gccccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg	540
	acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca	600
	aaacgtgcga gaaaatgaat cagaatttca acatttgctt cacgcacggg gtcagagact	660
20	gctcagaatg tttccccggg gcatcagaat ctcaaccggg cgtcagaaaa aaaacgtatc	720
	agaaactgtg tgccattcat catctgctgg ggcgggcacc cgagattgct tgctcggcct	780
	gcgatctggt caacgtggac ctggacgact gtgtttctga gcaataaatg acttaaacca	840
25	ggtatggctg ccgatggtta tcttccagat tggcttgagg acaacctctc tgagggcatt	900
	cgcgagtggt gggacctgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag	960
	gacgacggcc ggggtctggt gcttctctggc tacaagtacc tcggaccctt caacggactc	1020
30	gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac	1080
	gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag	1140
	tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcy agcagtcttc	1200
35	caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct	1260
	cctggaaaga agagaccggt agagccatca cctcagcgtt ccccgactc ctccacgggc	1320
	atcggcaaga aaggccacca gcccgcgaga aagagactga actttgggca gactggcgac	1380
40	tcggagtcag tccccgaccc tcaaccaatc ggagaaccac cagcaggccc ctctggtctg	1440
	ggatctggta caatggctgc aggcgggtggc gctccaatgg cagacaataa cgaaggcgcc	1500
	gacggagtggt gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga	1560

EP 1 310 571 B1

gtcatcacca ccagcaccgc aacctgggcc ctgcccacct acaacaacca tctctacaag 1620
caaattctcca acggggacatc gggaggaagc actaacgaca acacctactt tggctacagc 1680
5 accccctggg ggtatttttga cttcaacaga ttccactgcc acttctcacc acgtgactgg 1740
cagcgactca tcaacaataa ctgggggattc cggcccaaga gactcaactt caagctcttc 1800
aacatccagg tcaaggaggt cagcgagaat gaaggcacca agaccatcgc caataacctt 1860
10 accagcacga ttcagggtgtt tacggactcg gaataccagc tcccgtaegt ccccggtctt 1920
gcgccaccagg gctgcctccc tccgttcccc gcggaegtct tcatgattcc tcagtacggg 1980
tatctgaccc taaacaatgg cagtcagggt gtgggcccgtt cctccttcta ctgcctggaa 2040
15 tacttccctt ctcaaagtgt gaggacgggc aacaactttg aattcagcta caccttcgag 2100
gacgtgcctt tccacagcag ctacgcgcac agccagagcc tggaccgggt gatgaaccct 2160
ctcatcgacc agtacctgta ttacttatcc agaactcagt ccacaggagg aactcaagggt 2220
20 actcagcaat tgttattttc tcaagccggg cccgcaaaca tgtcggctca ggccaagaac 2280
tggctacctg gaccgtgtta ccgtcagcaa cgagtttcca cgacactgtc gcaaaacaac 2340
aacagcaatt ttgcttggac cgggtgccacc aagtatcacc tgaatggcag agactccctg 2400
25 gttaatcccg gcgttgccat ggctacccac aaggacgacg aggagcgctt cttcccgctca 2460
agcggagttc taatgtttgg caagcagggg gctggaaaag acaatgtgga ctacagcagc 2520
gtgatgctca ccagcgaaga agaaattaaa actactaacc cagtggctac agagcagtat 2580
30 ggtgtggtgg cagacaacct gcagcagacc aacggagctc ccattgtggg aactgtcaac 2640
agccaggggg ccttacctgg tatggtctgg caaaaccggg acgtgtacct gcagggcccc 2700
atctgggcca aaattcctca cacggacggc aactttcatc cttcgccgct gatgggaggg 2760
35 tttggactga aacaccgcgc tcctcagatc ctggtgaaaa acactcctgt tcctgcggat 2820
cctccgacca ccttcagcca ggccaagctg gcttctttta tcacgcagta cagcaccgga 2880
caggtcagcg tggaaatcga atgggagctg cagaaagaaa acagcaagcg ctggaacca 2940
40 gagattcagt atacttccaa ctactacaaa tctacaaatg tggactttgc tgtcaatact 3000
gagggctactt attcagagcc tcgccccatt ggcactcgtt atctcaccgc taatctgtaa 3060
45 ttgcttggtta atcaataaac cgggt 3084

<210> 40

<211> 2370

<212> DNA

50 <213> new AAV serotype, clone 43.5

<400> 40

55

EP 1 310 571 B1

	gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt	60
	gcgtcgacaa gatggtgatc tgggtgggagg agggcaagat gacggccaag gtcgtggagt	120
5	ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaagtgc aagtcgtccg	180
10		
15		
20		
25		
30		
35		
40		
45		
50		
55		

EP 1 310 571 B1

	cccagatcga cccacacccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg	240
	acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaagttcg	300
5	aactcaccgg ccgtctggag cactgactttg gcaaggtgac caagcaggaa gtcaaagagt	360
	tcttccgctg ggcgaggat cactgaccg aggtggcgca tgagtcttac gtcagaaagg	420
	gcgagaccag caaaagaccc gccccgatg acgcggatat aagcgagccc aagcgggcct	480
10	gcccctcagt cgcgatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg	540
	acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagacgctg tttccctgca	600
	aaacgtgcga gagaatgaat cagaatttca acatttgctt cactcacggg gtcagagact	660
15	gctcagaatg tttcccgggt gcatcagaat ctcaaccggt cgtcagaaaa aaaacgtatc	720
	agaaactgtg tgccattcat catctgctgg ggcgggcacc cgagattgct tgctcggcct	780
	gcgatctggg caacgtggac ctggacgact gtgtttctga gcaataaatg acttaaacca	840
20	ggtatggctg ccgatggta tcttccagat tggcttgagg acaacctctc tgagggcatt	900
	cgcgagtggg gggacctgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag	960
	gacgacggcc ggggtctggg gcttcctggc tacaagtacc tcggaccctt caacggactc	1020
25	gacaaggggg agcccgtaaa cgcgggcgac gcagcggccc tcgagcacga caaggcctac	1080
	gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag	1140
	tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc	1200
30	caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct	1260
	cctggaaaga agagaccggt agagccatca cctcagcgtt cccccgactc ctccacgggc	1320
	atcggcaaga aaggccacca gcccgcgaga aagagactga actttgggca gactggcgac	1380
35	tcggagttag tccccgaccc tcaaccaatc ggagaaccac cagcaggccc ctctggtctg	1440
	ggatctggtg caatggctgc aggcgggtggc gctccaatgg cagacaataa cgaaggcgcc	1500
	gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga	1560
40	gtcatcacca ccagcacccg aacctgggac ctgcccacct acaacaacca tctctacaag	1620
	caaatctcca acgggacatc gggaggaagc actaacgaca acacctactt tggctacagc	1680
	accccctggg ggtattttga cttcaacaga ttccactgcc acttctcacc acgtgactgg	1740
45	cagcgactca tcaacaataa ctggggattc cggcccaaga gactcaactt caagctcttc	1800
	aacatccagg tcaaggaggc cactgcagaat gaaggcacca agaccatcgc caataacctt	1860
	accagcacga ttcagggtgt tacggactcg gaataaccagc tcccgtacgt cctcggctct	1920
50	gcgcaccagg gctgcctccc tccgttcccg gcggacgtct tcatgattcc tcagtacggg	1980
	tatctgaccc taaacaatgg cagtcaggct gtggggcgtt cctccttcta ctgcctggaa	2040
55	tacttccctt ctcaaatgct gaggacgggc aacaactttg aattcagcta caccttcgag	2100

EP 1 310 571 B1

	gacgtgcctt tccacagcag ctacgcgcac agccagagcc tggaccgggt gatgaaccct	2160
5	ctcatcgacc agtacctgta ttacttatcc agaactcagt ccacaggagg aactcaaggt	2220
	actcagcaat tgttattttc tcaagccggg cccgcaaaca tgytgggtca ggccaagaac	2280
	tggctacctg gaccgtgtta ccgtcagcaa cgagtttcca cgacactgtc gcaaaacaac	2340
10	aacagcaatt ttgctggacc ggtgccacca	2370

	<210> 41
	<211> 3123
15	<212> DNA
	<213> new AAV serotype, clone 43.12
	<400> 41

20

25

30

35

40

45

50

55

EP 1 310 571 B1

	gaattcgccc ttggtgcgt caactggacc aatgagaact ttccttcaa cgattgcgtc	60
	gacaagatgg tgatctggtg ggaggagggc aagatgacgg ccaaggtcgt ggagtccgcc	120
5	aaggccattc tcggcggcag caagggtgcg gtggaccaa agtgcaagtc gtccgcccag	180
	atcgacccca ccccggtgat cgtcacctcc aacaccaaca tgtgcgccgt gattgacggg	240
	aaCagcacca ccttcgagca ccagcagccg ttgcaggacc ggatgttcaa gttcgaactc	300
10	acccgccgtc tggagcacga ctttggaag gtgaccaagc aggaagtcaa agagtcttc	360
	cgctggggcg aggatcacgt gaccgaggtg gcgcatgagt tctacgtcag aaagggcgga	420
	gccagcaaaa gaccgcgcc c gatgacgcg gatataagcg agcccaagcg ggcctgcccc	480
15	tcagtgcggg atccatcgac gtcagacgcg gaaggagctc cgggtggactt tgccgacagg	540
	tacaaaaaca aatgttctcg tcacggggc atgctccaga tgctgtttcc ctgcaaaacg	600
	tgcgagagaa tgaatcagaa tttcaacatt tgcttcacgc acgggggtcag agactgctca	660
20	gaatgtttcc ccggtgcatc agaattctcaa ccggtcgtca gaaaaaaaaac gtatcagaaa	720
	ctgtgtgcca ttcacatctt gctggggcg gcacccgaga ttgcttgctc ggcctgcgat	780
	ctggtcaacg tggacctgga cgactgtgtt tctgagcaat aaatgactta aaccagggtat	840
25	ggctgccgat ggttatcttc cagattggct tgaggacaac ctctctgagg gcattcgcga	900
	gtggtgggac ctgaaacctg gagccccgaa acccaaagcc aaccagcaaa agcaggacga	960
	cggccgggggt ctggtgcttc ctggctacaa gtacctcgga cccttcaacg gactcgacaa	1020
30	gggggagccc gtcaacgcgg cggacgcagc ggcctcgag cacgacaagg cctacgacca	1080
	gcagctcaaa gcgggtgaca atccgtacct gcggtataac cacgccgacg ccgagtttca	1140
	ggagcgtctg caagaagata cgtcttttgg gggcaacctc gggcgagcag tcttccaggc	1200
35	caagaagcgg gttctcgaac ctctcggtct ggttgaggaa ggcgctaaga cggtcctgg	1260
	aaagaagaga ccggtagagc catcacctca gcgttcccc gactcctcca cgggcatcgg	1320
	caagaaaggc caccagcccg cgagaaagag actgaacttt gggcagactg gcgactcgga	1380
40	gtcagtcccc gaccctcaac caatcgga accaccagca ggccctctg gtctgggatc	1440

EP 1 310 571 B1

	tggtacaatg gctgcaggcg gtggcgctcc aatggcagac aataacgaag gcgccgacgg	1500
	agtgggtagt tcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcac	1560
5	caccaccagc acccgaacct gggccctgcc cacctacaac aaccatctct acaagcaaat	1620
	ctccaacggg acatcgggag gaagcactaa cgacaacacc tactttggct acagcacc	1680
	ctgggggtat tttgacttca acagattcca ctgccacttc tcaccacgtg actggcagcg	1740
10	actcatcaac aataactggg gattccggcc caagagactc aacttcaagc tcttcaacat	1800
	ccagggtcaag gaggtcacgc agaataagag caccaagacc atcgccaata accttaccag	1860
	cacgattcag gtgtttacgg actcgggaata ccagctcccg tacgtcctcg gctctgcgca	1920
15	ccagggtcgc ctccctccgt tcccggcgga cgtcttcatg attcctcagt acgggtatct	1980
	gaccctaaac aatggcagtc aggctgtggg ccgttcctcc ttctactgcc tggaatactt	2040
	cccttctcaa atgctgagga cgggcaacaa ctttgaattc agctacacct tcgaggacgt	2100
20	gcctttccac agcagctacg cgcacagcca gagcctggac cggctgatga accctctcat	2160
	cgaccagtac ctgtattact tatccagaac tcagtccaca ggaggaaactc aaggtactca	2220
	gcaattgtta ttttctcaag ccgggcccgc aaacatgtcg gctcaggcca agaactggct	2280
25	acctggaccg tggtaccgtc agcaacgagt ttccacgaca ctgtcgcaaa acaacaacag	2340
	caattttgct tggaccgggtg ccaccaagta tcacctgaat ggcagagact ccctgggtta	2400
	tcccggcggt gccatggcta cccacaagga cgacgaggag cgcttcttcc cgtcaagcgg	2460
30	agtcttaatg tttggcaagc agggggctgg aaaagacaat gtggactaca gcagcgtgat	2520
	gctcaccagc gaagaagaaa ttaaaactac taaccagtg gctacagagc agtatgggtgt	2580
	ggtggcagac aacctgcagc agaccaacgg agctccatt gtgggaactg tcaacagcca	2640
35	gggggcctta cctgggtatg tctggcaaaa ccgggacgtg tacctgcagg gccccatctg	2700
	ggccaaaatt cctcacacgg acggcaactt tcacctctcg ccgctgatgg gaggttttg	2760
	actgaaacac ccgcctctc agatcctgg gaaaaacact cctgttctct cggtacctcc	2820
40	gaccaccttc agccaggcca agctggcttc ttttatcag cagtacagca ccggacaggt	2880
	cagcgtggaa atcgaatggg agctgcagaa agaaaacagc aagcgtgga acccagagat	2940
	tcagtatact tccaactact acaaactctac aaatgtggac tttgctgtca atactgaggg	3000
45	tacttattca gagcctcgcc ccattggcac tcgttatctc acccgtaatc tgtaattgct	3060
	tgtaaatcaa taaaccgggt aattcggttc agttgaactt tggctctctgc gaagggcgaa	3120
50	ttc	3123

<210> 42

<211> 3122

<212> DNA

55 <213> new AAV serotype, clone 43.20

<400> 42

EP 1 310 571 B1

gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60
 gcgtcgacaa gatggtgatc tggtagggagg agggcaagat gacggccaag gtcgtggagt 120
 5 ccgccaaggc cattctcggc ggcagcaagg tgcgtgtgga ccaaaagtgc aagtcttccg 180
 cccagatcga tcccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240
 acgggaacag cgccaccttc gagcaccagc agccgttgca ggaccggatg ttcaaatttg 300
 10 aactcaccgg ccgtctggag catgactttg gcaagggtgac gaagcaggaa gtcaaagagt 360
 tcttcgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttccac gtcagaaagg 420
 gtggagccaa caagagaccc gcccccgatg acgcggatat aagcgagccc aagcgggcct 480
 15 gcccctcagt cgcggtacca tcgacgtcag acgcggaaagg agctccggtg gactttgccg 540
 acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600
 agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660
 20 gttcagaatg tttccccggc gtgtcagaat ctcaaccggg cgtcagaaag aggacgtatc 720
 ggaaactctg tgcgattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780
 gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840
 25 ggtatggctg ccgatgggta tcttccagat tggctcgagg acaacctctc tgagggcatt 900
 cgcgagtggg gggacttgaa acctggagcc ccgaaaccca aagccaacca gaaaagcag 960
 gacgacggcc ggggtctggt gcttctctggc tacaagtacc tcggaccctt caacggactc 1020
 30 gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaagcctac 1080
 gaccagcagc tcaaagcggg tgacaatccg tacctgcggg ataatcacgc cgacgccgag 1140
 tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcggggc agcagtcttc 1200
 35 caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260
 cctggaaaga agagactggt agagcagtcg ccacaagagc cagactcctc ctcgggcatc 1320
 ggcaagacag gccagcagcc cgctaaaaag agactcaatt ttggtcagac tggcgactca 1380
 40 gagtcagtcc ccgaccaca acctctcgga gaacctccag cagccccctc aggtctggga 1440
 cctaatacaa tggcttcagg cggtaggcgt ccaatggcag acaataacga aggcgccgac 1500
 ggagtgggta attcctcggg aaattggcat tgcgattcca catggctggg ggacagagtc 1560
 45 atcaccacca gcaccgaac ctgggcccctg cccacctaca acaaccacct ctacaagcaa 1620
 atctccaacg gcacctcggg aggaagcacc aacgacaaca cctatttttg ctacagcacc 1680
 ccctgggggt attttgactt caacagattc cactgtcact tttcaccag tgactggcaa 1740
 50 cgactcatca acaacaattg gggattccgg cccaaaagac tcaacttcaa gctgttcaac 1800
 atccaggtca aggaagtcac gacgaacgaa ggcaccaaga ccatcgccaa taatctcacc 1860
 agcaccgtgc aggtctttac ggactcggag taccagttac cgtacgtgct aggatccgct 1920

55

EP 1 310 571 B1

	caccagggat gtctgcctcc gtccccggcg gacgtcttca cggttcctca gtacggctat	1980
	ttaacttttaa acaatggaag ccaagccctg ggacgttctt ccttctactg tctggagtat	2040
5	ttcccatcgc agatgctgag aaccggcaac aactttcagt tcagctacac cttegaggac	2100
	gtgccttttc acagcagcta cgcgcacagc cagagcctgg acaggctgat gaatccccctc	2160
	atcgaccagt acctgtacta cctggtcaga acgcaaacga ctggaactgg agggacgcag	2220
10	actctggcat tcagccaagc gggtcctagc tcaatggcca accaggctag aaattgggtg	2280
	cccggacctt gctaccggca gcagcgcgtc tccacgacaa ccaaccagaa caacaacagc	2340
	aactttgcct ggacgggagc tgccaagttt aagctgaacg gccgagactc tctaataaat	2400
15	ccgggcgtgg caatggcttc ccacaaggat gacgacgacc gcttcttccc ttcgagcggg	2460
	gtcctgattt ttggcaagca aggagccggg aacgatggag tggattacag ccaagtgctg	2520
	attacagatg aggaagaaat caaggctacc aaccccgctg ccacagaaga atatggagca	2580
20	gtggccatca acaaccaggc cgccaatacg caggcgcaga ccggactcgt gcacaaccag	2640
	ggggtgattc ccggcatggt gtggcagaat agagacgtgt acctgcaggg tcccatctgg	2700
	gccaaaattc ctcacacgga cggcaacttt caccgcgtct ccctgatggg cggtcttgga	2760
25	ctgaagcacc cgcctcctca aattctcatc aagaacacac cggttccagc ggaccgcgcg	2820
	cttaccttca accaggccaa gctgaactct ttcattcacgc agtacagcac cggacaggtc	2880
	agcgtggaaa tcgagtggga gctgcagaaa gaaaacagca aacgctggaa tccagagatt	2940
30	caatacactt ccaactacta caaatctaca aatgtggact ttgctgtcaa cacggaagga	3000
	gtttatagcg agcctcgccc cattggcacc cgttacctca cccgcaacct gtaattacat	3060
	gttaatcaat aaaccggtta attcgtttca gttgaacttt ggtctctgcg aagggcgaat	3120
35	tc	3122

<210> 43
 <211> 3117
 <212> DNA
 <213> new AAV serotype, clone 43.21

<400> 43

	gaattcgccc ttggctgctg caactggacc aatgagaact ttcccttcaa cgattgcgtc	60
	gacaagatgg tgatctggtg ggaggagggc aagatgacgg ccaaggctcg ggagtccgcc	120
50	aaggccattc tcggcggcag caaggctgct gtggaccaa agtgcaagtc ttccgcccag	180
	atcgatccca ccccgctgat cgtcacctcc aacaccaaca tgtgcgccgt gattgacggg	240
	aacagcacca ccttcgagca ccagcagccg ttgcaggacc ggatgttcaa atttgaactc	300
55	acccgccgtc tggagcatga ctttggaag gtgacgaagc aggaagtcaa agagttcttc	360
	cgctgggcgc aggatcacgt gaccgaggtg gcgcatgagt tccacgtcag aaagggtgga	420

EP 1 310 571 B1

	gccaacaaga gacccgcccc cgatgacgcg gatataagcg agcccaagcg ggcttgcccc	480
	tcagtcgchg atccatcgac gtcagacgcg gaaggagctc cggaggactt tgccgacagg	540
5	tacaaaaaca aatgtttctcg tcacgcgggc atgcttcaga tgctgtttcc ctgcaagaca	600
	tgcgagagaa tgaatcagaa tttcaacatt tgcttcacgc acgggaccag agactgttca	660
10	gaatgtttcc ccggcggtgc agaattctcaa ccggctcgta gaaagaggac gtatcgga	720
	ctctgtgcga ttcatcatct gctggggcgg gctcccgaga ttgcttgctc ggcttgcat	780
	ctgggtcaacg tggacctgga tgactgtgtt tctgagcaat aaatgactta aaccaggat	840
15	ggctgcccgt gggttatcttc cagattggct cgaggacaac ctctctgagg gcattcgca	900
	gtgggtgggac ttgaaacctg gagccccgaa acccaaagcc aaccagcaaa agcaggacga	960
	cggccgggggt ctgggtgcttc ctgggtacaa gtacctcgga cccttcaacg gactcgacaa	1020
20	gggggagccc gtcaacgcgg cggacgcagc ggccctcgag cagacaaag cctacgacca	1080
	gcagctcaaa gcgggtgaca atccgtacct gcggtataat cagccgacg ccgagtttca	1140
	ggagcgtctg caagaagata cgtcttttgg gggcaacctc gggcgagcag tcttccaggc	1200
25	caagaagcgg gttctcgaac ctctcggctt gggtgaggaa ggcgctaaga cggctcctgg	1260
	aaagaagaga ccggtagagc agtcgccaca agagccagac tcctcctcgg gcacggcaa	1320
	gacaggccag cagcccgtta aaaagagact caattttggg cagactggcg actcagagtc	1380
30	agtccccgac ccacaacctc tcggagaacc tcagcagcc ccctcaggct tgggacctaa	1440
	tacaatggct tcaggcgggtg gcgctccaat ggcagacaat aacgaaggcg ccgacggagt	1500
	gggtaattcc tcgggaaatt ggcattgcga ttccacatgg ctgggggaca gagtcatac	1560
35	caccagcacc cgaacctggg ccctgcccac ctacaacaac cacctctaca agcaaattctc	1620
	caacggcacc tcgggaggaa gcaccaacga caacacctat tttggctaca gcacccctg	1680
	gggggtatatt gacttcaaca gattccactg tcacttttca ccacgtgact ggcaacgact	1740
40	catcaacaac aattggggat tccggcccaa aagactcaac ttcaagctgt tcaacatcca	1800
	ggtcaaggaa gtcacgacga acgaaggcac caagaccatc gccaataatc tcaccagcac	1860
	cgtgcgggtc ttacaggact cggagtacca gttaccgtac gtgctaggat ccgctacca	1920
45	gggatgtctg cctccgttcc cggcgagcgt cttcatgggt cctcagtagc gctatttaac	1980
	tttaaacaat ggaagccaag ccctgggacg ttctctcttc tactgtctgg agtatttccc	2040
	atcgagatg ctgagaaccg gcaacaactt tcagttcagc tacaccttcg aggacgtgcc	2100
50	tttccacagc agctacgcgc acagccagag cctggacagg ctgatgaatc ccctcatcga	2160
	ccagtacctg tactacctgg tcagaacgca aacgactgga actggaggga cgcagactct	2220
	ggcattcagc caagcgggtc ctagctcaat ggccaaccag gctagaaatt ggggtcccgg	2280
55	accttgctac cggcagcagc gcgtctccac gacaaccaac cagagcaaca acagcaactt	2340

EP 1 310 571 B1

	tgcctggacg	ggagctgcca	agtttaagct	gaacggccga	gactctctaa	tgaatccggg	2400
	cgtggcaatg	gcttcccaca	aggatgacga	cgaccgcttc	ttcccttcga	gcgggggtcct	2460
5	gattttttggc	aagcaaggag	cggggaacga	tggagtggat	tacagccaag	tgctgattac	2520
	agatgaggaa	gaaatcaagg	ctaccaaccc	cgtggccaca	gaagaatatg	gagcagtggc	2580
10	catcaacaac	caggccgcca	atacgcaggc	gcagaccgga	ctcgtgcaca	accaggggggt	2640
	gattccccggc	atggtgtggc	agaatagaga	cgtgtacctg	caggggtccca	tctggggccaa	2700
	aattcctcac	acggacggca	actttcaccc	gtctcccctg	atgggagggt	ttggactgaa	2760
15	gcacccgcct	cctcaaattc	tcatcaagaa	cacaccggtt	ccagcggacc	cgccgcttac	2820
	cttcaaccag	gccaaagtga	actctttcat	cacgcagtac	agcaccggac	aggtcagcgt	2880
	ggaaatcgag	tgggagctgc	agaaagaaaa	cagcaaacgc	tggaatccag	agattcaata	2940
20	cacttccaac	tactacaaat	ctacaaatgt	ggactttgct	gtcaacacgg	aaggagttaa	3000
	tagcgagcct	cgccccattg	gcaccggtta	cctcaccgcg	aacctgtaat	tacatgttaa	3060
	tcaataaacc	ggttaattcg	tttcagttga	actttggtct	ctgcgaaggg	cgaattc	3117

25

<210> 44
 <211> 3121
 <212> DNA
 <213> new AAV serotype, clone 43.23

30

<400> 44

35

40

45

50

55

EP 1 310 571 B1

gaattcgccc ttctacggct gcgtcaactg gaccaatgag aactttccct tcaacgattg 60
 cgtcgacaag atggtgatct ggtgggagga gggcaagatg acggccaagg tcgtggagtc 120
 5 cgccaaggcc attctcggcg gcagcaaggc gcgtgtggac caaaagtgc agtcttccgc 180
 ccagatcgat cccacccccg tgatcgtcac ctccaacacc aacatgtgcg ccgtgattga 240
 cgggaacagc accaccttcg agcaccagca gccgttgacg gaccggatgt tcaaatttga 300
 10 actcaccgc cgtctggagc atgacttttg caaggtgacg aagcaggaag tcaaagagtt 360
 cttccgctgg gcgcaggatc acgtgaccga ggtggcgcat gagttccacg tcagaaaggg 420
 tggcgccaac aagagaccgc ccccgatga cgcgatata agcgagccca agcgggcctg 480
 15 cccctcagtc gcggatccat cgacgtcaga cgcggaagga gctccggtgg actttgccga 540
 caggtaccaa aacaaatgtt ctcgtcacgc gggcatgctt cagatgctgt ttccctgcaa 600
 gacatgcgag agaatgaatc agaatttcaa catttgcttc acgcacggga ccagagactg 660
 20 ttcagaatgt ttccccggcg tgtcagaatc tcaaccggtc gtcagaaaga ggacgtatcg 720
 gaaactctgt gcgattcatc atctgctggg gcgggctccc gagattgctt gctcggcctg 780
 cgatctggtc aacgtggacc tggatgactg tgtttctgag caataaatga cttaaaccag 840
 25 gtatggctgc cgatgggtat cttccagatt ggctcgagga caacctctct gagggcattc 900
 gcgagtgggtg ggacttgaaa cctggagccc cgaaacccaa agccaaccag caaaagcagg 960

30

35

40

45

50

55

EP 1 310 571 B1

	acgacggccg ggggtctggtg cttcctggct acaagtacct cggacccttc aacggactcg	1020
	acaaggggga gcccgtaac gggcgggacg cagcgggccct cgagcacgac aaagcctacg	1080
5	accagcagct caaagcgggt gacaatccgt acctgcggta taatcacgcc gacgccgagt	1140
	ttcaggagcg tctgcaagaa gatacgtcct ttggggggcaa cctcggggcga gcagtcttcc	1200
	aggccaagaa gcgggttctc gaacctctcg gtctggttga ggaaggcgct aagacggctc	1260
10	ctggaaagaa gagaccggtg gagcagtcgc cacaagagcc agactcctcc tcgggcatcg	1320
	gcaagacagg ccagcagccc gctaaaaaga gactcaattt tggtcagact ggcgactcag	1380
	agtcagtccc cgaccacaaa cctctcggag aacctccagc agccccctca ggtctgggac	1440
15	ctaatacaat ggcttcaggc ggtggcgctc caatggcaga caataacgaa ggcgccgacg	1500
	gagtgggtaa ttcctcggga aattggcatt gcgattccac atggctgggg gacagagtca	1560
	tcaccaccag caccgaacc tgggccctgc ccacctacaa caaccacctc tacaagcaaa	1620
20	tctccaacgg cacctcggga ggaagcacca acgacaacac ctattttggc tacagcacc	1680
	cctgggggta ttttgacttc aacagattcc actgtcactt ttcaccacgt gactggcaac	1740
	gactcatcaa caacaattgg ggattccggc caaaagact caacttcaag ctgttcaaca	1800
25	tccaggtcaa ggaagtcacg acgaacgaag gcaccaagac catcgccaat aatctcacca	1860
	gcaccgtgca ggtcttttacg gacttgagat accagttacc gtacgtgcta ggatccgctc	1920
	accagggatg tctgcctccg ttcgccggcg acgtcttcac ggttcctcag tacggctatt	1980
30	taactttaaa caatggaagc caagccctgg gacgttcctc cttctactgt ctggagtatt	2040
	tcccatcgca gatgccgaga accggcaaca actttcagtt cagctacacc ttcgaggacg	2100
	tgccctttcca cagcagctac gcgcacagcc agagcctgga caggctgatg aatccccctca	2160
35	tcgaccagta cctgtactac ctggtcagaa cgcaaacgac tggaactgga gggacgcaga	2220
	ctctggcatt cagccaagcg ggtcctagct caatggccaa ccaggctaga aattgggtgc	2280
	ccggaccttg ctaccggcag cagcgcgtct ccacgacaac caaccagaac aacaacagca	2340
40	actttgcctg gacgggagct gccaaagtta agctgaacgg ccgagactct ctaatgaatc	2400
	cgggcgtggc aatggcttcc cacaaggatg acgacgaccg cttcttccct tcgagcgggg	2460
	tcctgathtt tggcaagcaa ggagccggga acgatggagt ggattacagc caagtgcgtga	2520
45	ttacagatga ggaagaaatc aaggctacca accccgtggc cacagaagaa tatggagcag	2580
	tggccatcaa caaccaggcc gccaatagc aggcgcagac cggactcgtg cacaaccagg	2640
	gggtgattcc cggcatgggtg tggcagaata gagacgtgta cctgcagggg cccatctggg	2700
50	ccaaaattcc tcacacggac ggcaactttc acccgtctcc cctgatgggc ggctttggac	2760
	tgaagcacc gcctcctcaa attctcatca agaacacacc ggttccagcg gaccgcgcg	2820
55	ttaccttcaa ccaggccaag ctgaactctt tcatcacgca gtacagcacc ggacaggtca	2880

EP 1 310 571 B1

	gcgtggaaat cgagtgggag ctgcagaaaag aaaacagcaa acgctggaat ccagagattc	2940
	aatacacttc caactactac aaatctacaa atgtggactt tgctgtcaac acggaaggag	3000
5	tttatagcga gcctcgcccc attggcacc cgttacctcac ccgcaacctg taattacatg	3060
	ttaatcaata aaccgggttaa ttcgttttcag ttgaactttg gtctctgcga agggcgaatt	3120
	c	3121
10	<210> 45 <211> 3122 <212> DNA <213> new AAV serotype, clone 43.25	
15	<400> 45	
	gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt	60
20	gcgtcgacaa gatggtgatc tgggtgggagg agggcaagat gacggccaag gtcgtggagt	120
	ccgccaaggc cattctcggc ggcagcaagg tgcgtgtgga ccaaaagtgc aagtcttccg	180
	cccagatcga tcccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg	240
25	acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaaatttg	300
	aactcaccgc ccgtctggag catgactttg gcaagggtgac gaagcaggaa gtcaaagggg	360
	tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagtccac gtgcgagccc	420
30	aagcgggcct gcccctcagt cgcggatcca tcgacgtcag accagaaagg gtggagccaa	480
	caagagaccc gcccccgatg acgcggatat aagcgggaagg agctccgggtg gactttgccg	540
	acaggtagca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca	600
35	agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact	660
	gttcagaatg tttccccggc gtgtcagaat ctcaaccggg cgtcagaaag aggacgtatc	720
	ggaaactctg tgcgattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct	780
40	gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca	840
	ggtatggctg ccgatgggta tcttccagat tggctcgagg acaacctctc tgagggcatt	900
	cgcgagtggg gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag	960
45	gacgacggcc ggggtctggt gcttccctggc tacaagtacc tcggaccctt caacggactc	1020
	gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaagcctac	1080
	gaccagcagc tcaaagcggg tgacaatccg tacctgcggg ataatcacgc cgacgccgag	1140
50	tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcggggc agcagtcttc	1200
	caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct	1260
	cctggaaaga agagaccggt agagcagtcg ccacaagagc cagactcctc ctcgggcatc	1320
55	ggcaagacag gccagcagcc cgctaaaaag agactcaatt ttggtcagac tggcgactca	1380
	gagtcagtcc ccgaccaca acctctcgga gaacctccag cagccccctc aggtctggga	1440

EP 1 310 571 B1

	cctaatacaa tggcttcagg cggtggcgct ccaatggcag acaataacga aggcgccgac	1500
	ggagtgggta attcctcggg aaattggcat tgcgattcca catggctggg ggacagagtc	1560
5	atcaccacca gcaccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa	1620
	atctccaacg gcacctcggg aggaagcacc aacgacaaca cctatttttg ctacagcacc	1680
	ccctgggggt attttgactt caacagattc cactgtcact tttcaccacg tgactggcaa	1740
10	cgactcatca acaacaattg gggattccgg cccaaaagac tcaacttcaa gctgttcaac	1800
	atccagggtca aggaagtcac gacgaacgaa ggcaccaaga ccatcgccaa taatctcacc	1860
	agcaccgtgc aggtctttac ggactcggag taccagttac cgtacgtgct aggatccgct	1920
15	caccagggat gtctgcctcc gttcccgggc gacgtcttca tggttcctca gtacggctat	1980
	ttaactttaa acaatggaag ccaagccctg ggacgttctt ccttctactg tctggagtat	2040
	ttcccatcgc agatgctgag aaccggcaac aactttcagt tcagctacac cttcgaggac	2100
20	gtgcctttcc acagcagcta cgcgcacagc cagagcctgg acaggctgat gaatccccctc	2160
	atcgaccagt acctgtacta cctgggtcaga acgcaaacga ctggaactgg agggacgcag	2220
	actctggcat tcagccaagc gggtcctagc tcaatggcca accaggctag aaattgggtg	2280
25	cccgacctt gctaccggca gcagcgcgtc tccacgacaa ccaaccagaa caacaacagc	2340
	aactttgcct ggacgggagc tgccaagttt aagctgaacg gccgagactc tctaataaat	2400
	ccgggcggtg caatggcttc ccacaaggat gacgacgacc gcttcttccc ttcgagcggg	2460
30	gtcctgattt ttggcaagca aggagccggg aacgatggag tggattacag ccaagtgctg	2520
	attacagatg aggaagaaat caaggctacc aaccccgtag ccacagaaga atatggagca	2580
	gtggccatca acaaccaggc cgccaatacg caggcgcaga ccggactcgt gcacaaccag	2640
35	ggggtgattc ccggcatggt gtggcagaat agagacgtgt acctgcaggg tcccatctgg	2700
	gccaaaattc ctcacacgga cggcaacttt caccgctctc ccctgatggg cggctttgga	2760
	ctgaagcacc cgcctcctca aattctctatc aagaacacac cggttccagc ggacccgccg	2820
40	cttaccttca accaggccaa gctgaactct ttcacacgc agtacagcac cggacaggtc	2880
	agcgtggaaa tcgagtggga gctgcagaaa gaaaacagca aacgctggaa tccagagatt	2940
	caatacactt ccaactacta caaatctaca aatgtggact ttgctgtcaa cacggagggg	3000
45	gtttatagcg agcctcgccc cattggcacc cgttacctca cccgcaacct gtaattacat	3060
	gttaatcaat aaaccggtta attcgtttca gttgaacttt ggtctctgcg aagggcgaat	3120
50	tc	3122

<210> 46

<211> 3128

<212> DNA

55 <213> new AAV serotype, clone 44.1

<400> 46

EP 1 310 571 B1

	gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt	60
	gcgtcgacaa gatgttgatc tgggtgggagg agggcaagat gacggccaag gtcgtggagt	120
5	ccgccaaaggc cattctcggc ggcagcaaaag tgcgcgtgga ccaaaagtgc aagccgtccg	180
	cccagatcga ccccccacccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg	240
	acgggaacag caccaccttc gagcaccagc agccgttgcg ggaccggatg ttcaagtttg	300
10	aactcaccgg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcagagagt	360
	tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca cgagttctac gtcagaaagg	420
	gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct	480
15	gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg	540
	acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca	600
	aaacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact	660
20	gttcagaatg tttccccggc gtgtcagaat ctcaaccggg cgtcagaaaa aagacgtatc	720
	ggaaactctg tgcgattcat catctgctgg ggcgggcacc cgagattgct tgctcggcct	780
	gcgatctggt caacgtggac ctagatgact gtgtttctga gcaataaatg acttaaacca	840
25	ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt	900
	cgcgagtggg gggacttgaa acctggagcc ccgaaacca aagccaacca gcaaaagcag	960
	gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc	1020
30	gacaaggggg agcccgtaaa cgcggcggac gcagcggccc tcgagcacga caaggcctac	1080
	gaccagcagc tcaaagcggg tgacaatccg tacctgcggg ataaccacgc cgacgccgag	1140
	tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc	1200
35	caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct	1260
	cctggaaaga agagaccggg agagccatca cccagcgtt ctccagactc ctctacgggc	1320
	atcggcaaga aaggccagca gcccgcgaaa aagagactca actttgggca gactggcgac	1380
40	tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg	1440
	ggatctggta caatggctgc aggcgggtggc gctccaatgg cagacaataa cgaaggcgcc	1500
	gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga	1560
45	gtcatcacca ccagcacccg aacctgggccc ctccccacct acaacaacca cctctacaag	1620
	caaatctcca acgggacttc gggaggaagc accaacgaca acacctactt cggctacagc	1680
	acccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg	1740
50	cagcgactca tcaacaacaa ctggggattc cggcccaaga gactcaactt caagctcttc	1800
	aacatccagg tcaaggaggc cacgcagaat gaaggcacca agaccatcgc caataacctt	1860
55	accagcacga ttcagggtctt tacggactcg gaataccagc tcccgtacgt cctcggctct	1920

EP 1 310 571 B1

	gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg	1980
	tacctgactc tgaacaatgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag	2040
5	tactttcctt ctcaaagtgt gagaacgggc aacaactttg agttcagcta ccagtttgag	2100
	gacgtgcctt ttacacagcag ctacgcgcac agccaaagcc tggaccggct gatgaacccc	2160
	ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga	2220
10	actcagcagt tgctattttc tcaggccggg cctaataaca tgtcggctca ggccaaaaac	2280
	tggctacccg ggccctgcta ccggcagcaa cgcgctctcca cgacactgtc gcaaaataac	2340
	aacagcaact gtaaatcccg gtgtcgctat ggcaaccac aaggacgacg aagagcgatt	2400
15	ttgcctggac cggtgccacc aagtatcatc tgaatggcag agactctctg ttttccgtcc	2460
	agcggagtct taatgtttgg gaaacaggga gctggaaaag acaacgtgga ctatagcagc	2520
	gttatgctaa ccagttagga agaaattaaa accaccaacc cagtggccac ggaacagtac	2580
20	ggcgtggtgg ccgataacct gcaacagcaa aacgccgctc ctattgtagg ggccgtcaac	2640
	agtcaaggag ccttacctgg catggtctgg cagaaccggg acgtgtacct gcagggtcct	2700
	atctgggcca agattcctca cacggacgga aactttcatc cctcgccgct gatgggaggc	2760
25	tttgactga aacacccgcc tcctcagatc ctgattaaga atacacctgt tcccgcggat	2820
	cctccaacta ccttcagtca agctaagctg gcgtcgttca tcacgcagta cagcaccgga	2880
	caggtcagcg tggaaattga atgggagctg cagaaagaaa acagcaaacg ctggaacca	2940
30	gagattcaat acaattccaa ctactacaaa tctacaaatg tggacttcgc tgttaacaca	3000
	gatggcactt attctgagcc tcgccccatt ggcacccggt acctcaccg taatctgtaa	3060
	ttgctcgtaa atcaataaac cggttgattc gtttcagttg aactttgggtc tctgcgaagg	3120
35	gcgaattc	3128

<210> 47

<211> 3128

40 <212> DNA

<213> new AAV serotype, clone 44.5

<400> 47

45	gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt	60
	gcgtcgacaa gatggtgatc tggtagggagg agggcaagat gacggccaag gtcgtggagt	120
	ccgccaaggc cattctcggc ggcagcaaag tgcgcgtgga ccaaagtgac aagtcgtccg	180
50	cccagatcga cccaccccc gtgatcgta cctccaacac caacatgtgc gccgtgattg	240
	acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaagtttg	300
	aactcaccgg ccgtctggag cagcactttg gcaagggtgac aaagcaggaa gtcagagagt	360
55	tcttccgctg ggccgaggat cacgtgaccg aggtggcgca cgagttctac gtcagaaagg	420
	gtggagccaa caagagaccc gccccgatg acgcggataa aagcgagccc aagcgggcct	480

EP 1 310 571 B1

	gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccc	540
	acagggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca	600
5	aaacatgcga gagaatgaat cagaatttca acattttgctt cacgcacggg accagagact	660
	gttcagaatg tttccccggc gtgtcagaat ctcaaccggt tgtcagaaaa aagacgtatc	720
10	ggaaactctg tgcgattcat catctgctgg ggccggccacc cgagattgct tgctcggcct	780
	gcgatctggt caacgtggac ctagatgact gtgtttctga gcaataaatg acttaaacca	840
	ggatatggctg ccgatgggta tcttcacgat tggctcgagg acaacctctc tgagggcatt	900
15	cgcgagtggg gggacttgaa acctggagcc ccgaaacca aagccaacca gcaaaagcag	960
	gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc	1020
	gacaaggggg agcccgtaaa cgcggcggac gcagcggccc tcgagcacga caaggcctac	1080
20	gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag	1140
	tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcggggc agcagtcttc	1200
	caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct	1260
25	cctggaaaga agagaccggt agagccatca cccagcgtt ctccagactc ctctacgggc	1320
	atcggcaaga aaggccagca gcccgcgaaa aagagactca actttgggca gactggcgac	1380
	tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctgggtctg	1440
30	ggatctggta caatggctgc aggcgggtggc gctccaatgg cagacaataa cgaaggcgcc	1500
	gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga	1560
	gtcatcacca ccagcaccgc aacctgggccc ctccccacct acaacaacca cctctacaag	1620
35	caaatctcca acgggacttc gggaggaagc accaacgaca acacctactt cggctacagc	1680
	acccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg	1740
	cagcgactca tcaacaacaa ctggggattc cggccaaga gacccaactt caagctcttc	1800
40	aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt	1860
	accagcacga ttcaggctct tacggactcg gaataccagc tcccgtagct cctcggctct	1920
	gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg	1980
45	tacctgactc tgaacaatgg cagtcaggcc gtgggcccgtt cctccttcta ctgcctggag	2040
	tactttcctt ctcaaagtgt gagaacgggc aacaactttg agttcagcta ccagtttgag	2100
	gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gatgaacccc	2160
50	ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga	2220
	actcagcagt tgctattttc tcaggccggg cctaataaca tgtcgggtca ggccaaaaac	2280
	tggctacccg ggccctgcta ccggcagcaa cgcgtctcca cgacactgtc gcaaaataac	2340
55	aacagcaact ttgcctggac cgggtgccacc aagtatcatc tgaatggcag agactctctg	2400

EP 1 310 571 B1

	gtaaatcccg gtgtcgctat ggcaaccac aaggacgacg aagagcgatt ttttccgtcc	2460
	agcggagtct taatgtttgg gaaacagggg gctggaaaag acaacgtgga ctatagcagc	2520
5	gttatgctaa ccagtgagga agaaattaaa accaccaacc cagtggccac agaacagtac	2580
	ggcgtggtgg ccgataacct gcaacagcaa aacgccgctc ctattgtagg ggccgtcaac	2640
	agtcaaggag ccttacctgg catggtctgg cagaaccggg acgtgtacct gcagggtcct	2700
10	atctggggcca agattcctca cacggacgga aactttcatc cctcgccgct gatgggaggc	2760
	tttggactga aacaccgccc tcctcagatc ctgattaaga atacacctgt tcccgcggtat	2820
	cctccaacta ccttcagtca agctaagctg gcgtcggttca tcacgcagta cagcaccgga	2880
15	caggtcagcg tggaaattga atgggagctg cagaaagaaa acagcaaacg ctggaaccga	2940
	gagattcaat acacttccaa ctactacaaa tctacaaatg tggactttgc tggttaacaca	3000
	gatggcactt attctgagcc tcgccccatt ggcaccggtt acctcaccgg taatctgtaa	3060
20	ttgcttggtta atcaataaac cggttgatcc gtttcagttg aactttgggc tctgcgaagg	3120
	gcgaattc	3128

25	<210> 48
	<211> 1933
	<212> DNA
	<213> new AAV serotype, clone 223.10
30	<220>
	<221> misc_feature
	<222> (1302)..(1302)
	<223> can be a, c, g or t
35	<400> 48

40

45

50

55

EP 1 310 571 B1

	caaggcctac	gaccagcagc	tcaaagcggg	tgacaatccg	tacctgcggt	ataaccacgc	60
	cgacgccgag	tttcaggagc	gtcttcaaga	agatacgtct	tttgggggca	acctcgggcg	120
5	agcagtcttc	caggccaaaa	agcgggttct	cgaacctctt	ggtctggttg	agacgccagc	180
	taagacggca	cctggaaaga	agcgaccggt	agactcgcca	gactccacct	cgggcatcgg	240
	caagaaaggc	cagcagcccc	cgaaaaagag	actcaacttt	gggcagactg	gcgactcaga	300
10	gtcagtcccc	gaccctcaac	caatcgga	accaccagca	ggcccctctg	gtctgggatac	360
	tgggtacaatg	gctgcaggcg	gtggcgacc	aatggctgac	aataacgagg	gcgccgacgg	420
	agtgggtaat	gcctcaggaa	attggcattg	cgattccaca	tggctgggcg	acagagtcac	480
15	caccaccagc	acccgaacct	gggccctgcc	cacctacaac	aaccacctct	acaagcaa	540
	ctccagtcag	tcagcaggga	gcaccaacga	taacgtctat	ttcggctaca	gcacccccctg	600
	ggggtatattt	gacttcaaca	gattccattg	ccacttctca	ccacgtgact	ggcagcgact	660
20	tatcaacaac	aactggggat	tccggcccaa	gaagctcaac	ttcaagctct	tcaacatcca	720
	ggtcaaggag	gtcacgacga	atgacggtgt	cacaaccatc	gctaataacc	ttaccagcac	780
25							
30							
35							
40							
45							
50							
55							

EP 1 310 571 B1

5
 10
 15
 20
 25
 30
 35

ggttcaggtc	ttttcggact	cggaatatca	actgccgtac	gtcctcggct	ccgcgcacca	840
gggctgcctg	cctccgttcc	cggcagacgt	gttcatgatt	ccgcagtagc	gatacctgac	900
tctgaacaat	ggcagccaat	cggtaggccc	ttcctccttc	tactgcctgg	agtactttcc	960
ttctcagatg	ctgagaacgg	gcaacaactt	caccttttagc	tacaccttcg	aggacgtgcc	1020
tttccacagc	agctacgcgc	acagccagag	tctggaccgg	ctgatgaatc	ccctcatcga	1080
ccagtacctg	tactacttgg	ccagaacaca	gagcaacgca	ggaggtagctg	ctggcaatcg	1140
ggaactgcag	ttttatcagg	gctggacctac	caccatggcc	gaacaagcaa	agaactggct	1200
gcccggacct	tgcttccggc	aacagagagt	atccaagacg	ctggatcaaa	ataacaacag	1260
caactttgcc	tggaactggg	ccacaaaata	ccattttaaat	gnaagaaatt	cattgggttaa	1320
tcccgggtgc	gccatggcaa	cccacaagga	cgacgaggaa	cgcttcttcc	cttcgagcgg	1380
agtttctaatt	tttggcaaaa	ctggagcagc	taataaaaact	acattagaaa	acgtgctcat	1440
gacaaatgaa	gaagaaattc	gtcctaccaa	cccggtagct	accgaggaat	acgggattgt	1500
aagcagcaac	ttgcaggcgg	ctagcaccgc	agcccagaca	caagttgtta	acaaccaggg	1560
agccttacct	ggcatggtct	ggcagaaccg	ggacgtgtac	ctgcaaggtc	ccatttgggc	1620
caagattcct	cacacggacg	gcaactttca	cccgtctcct	ctaattgggtg	gctttggact	1680
gaaacacccg	cctccccaga	tcctgatcaa	aaacacaccg	gtacctgcta	atcctccaga	1740
agtgtttact	cctgccaagt	ttgcttcctt	catcacgcag	tacagcaccg	ggcaagtcag	1800
cgttgagatc	gagtgggagc	tgcaaaaaga	gaacagcaag	cgctggaacc	cagagattca	1860
gtacacctcc	aactttgaca	aacagactgg	agtggacttt	gctgttgaca	gccagggtgt	1920
ttactctgag	cct					1933

<210> 49

<211> 1933

<212> DNA

<213> new AAV serotype, clone 223.2

<400> 49

EP 1 310 571 B1

	caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc	60
	cgacgccgag tttcaggagt gtcttcaaga agatacgtct ttgggggca acctcgggcg	120
5	agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc	180
	taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg	240
	caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga	300
10	gtcagtcccc gacctcaac caatcggaga accaccagca gggccctctg gtctgggatc	360
	tgggtacaatg gttgcaggcg gtggcgccacc aatggctgac aataacgagg gcgccgacgg	420
	agtgggtaat gcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcac	480
15	caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaa	540

20

25

30

35

40

45

50

55

EP 1 310 571 B1

	ctccagtcag tcagcagggg gcaccaacga taacgtctat ttcgggtaca gcacccctg	600
	gggggtatttt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact	660
5	tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca	720
	gggtcaaggag gtcacgacga atgacggtgt cacaaccatc gctaataacc ttaccagcac	780
	gggttcagggtc ttttcggact cgggaatatca actgccgtac gtcctcggct ccgcgcacca	840
10	gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtagc gatacctgac	900
	tctgaacaat ggcagccaat cggtagggcg ttcctccttc tactgcctgg agtactttcc	960
	ttctcagatg ctgagaacgg gcaacaactt caccttttagc tacaccttcg aggacgtgcc	1020
15	tttccacagc agctacgcgc acagccagag tctggaccgg ctgatgaatc ccctcatcga	1080
	ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg	1140
	ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct	1200
20	gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag	1260
	caactttgcc tggactggtg ccacaaaata ccatttaaatt ggaagaaatt cattgggttaa	1320
	tcccgggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttctccc cttcgagcgg	1380
25	agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat	1440
	gacaaatgaa gaagaaattc gtcctaccaaa cccggtagct accgaggaat acgggattgt	1500
	aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg	1560
30	agccttacct ggcatgggtc ggcagaaccg ggacgtgtac ctgcaaggct ccatttgggc	1620
	caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact	1680
	gaaacacccg cctccccaga tcctgatcaa aaacacgccg gtacctgcta atcctccaga	1740
35	agtgtttact cctgccaaagt ttgcttcctt catcacgcag tacagcaccg ggcaagtcag	1800
	cgttgagatc gagtgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca	1860
	gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt	1920
40	ttactctgag cct	1933

<210> 50

<211> 1933

<212> DNA

<213> new AAV serotype, clone 223.4

<400> 50

EP 1 310 571 B1

	caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc	60
	cgacgccgag tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg	120
5	agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc	180
	taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg	240
	caagaaaggc cagcagcccc cgaaaaagag actcaacttt gggcagactg gcgactcaga	300
10		
	gccagtcccc gacctcaac caatcggaga accaccagca ggccccctctg gtctgggatac	360
	tgggtacaatg gctgcaggcg gtggcgacc aatggctgac aataacgagg gcgccgacgg	420
15	agtgggtaat gcctcaggaa attggcattg cgattccaca cggctgggcg acagagtcac	480
	caccaccagc acccgaacct gggccccgcc cacctacaac aaccacctct acaagcaaat	540
	ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcacccccctg	600
20	ggggtatattt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact	660
	tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca	720
	ggtcaaggag gtcacgacga atgacggcgt cacaaccatc gctaataacc ttaccagcac	780
25	ggttcaggtc ttttcggact cggaatatca actgccgtac gtccctcggct ccgcgcacca	840
	gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtagc gatacctgac	900
	tctgaacaat ggcagccaat cggtagggcg ttcctccttc tactgcctgg agtactttcc	960
30	ttctcagatg ctgagaacgg gcaacaactt caccttttagc tacaccttcg aggacgtgcc	1020
	tttccacagc agctacgcgc acagccagag tctgggccgg ctgatgaatc ccctcatcga	1080
	ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtagct ctggcaatcg	1140
35	ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct	1200
	gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag	1260
	caactttgcc tggactggtg ccacaaaata ccattttaat ggaagaaatt cattgggttaa	1320
40	tcccgggtgc gccatggcaa ccacaaagga cgacgaggaa cgcttcttcc cttcgagcgg	1380
	agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat	1440
	gacaaatgaa gaagaaattc gtcctaccaa cccggtagct accgaggaat acgggattgt	1500
45	aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg	1560
	agccttacct ggcattggtct ggcagaaccg ggacgtgtac ctgcaaggtc ccatttgggc	1620
	caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact	1680
50	gaaacacccg cctccccaga tcctgatcaa aaacacaccg gtacctgcta atcctccaga	1740
	agtgtttact cctgccaaagt ttgcttcctt catcacgcag tacagcaccg ggcaagtcag	1800
	cgttgagatc gaatgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca	1860
55	gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt	1920
	ttactctgag cct	1933

EP 1 310 571 B1

<210> 51

<211> 1933

<212> DNA

<213> new AAV serotype, clone 223.5

5

<400> 51

caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc 60

10

15

20

25

30

35

40

45

50

55

EP 1 310 571 B1

	cgacgccgag tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg	120
	agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc	180
5	taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg	240
	caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga	300
10	gccagtcccc gacctcaac caatcggaga accaccagca ggccccctctg gtctgggatac	360
	tgggtacaatg gctgcaggcg gtggcgacc aatggctgac aataacgagg gcgccgacgg	420
	agtgggtaat gcctcaggaa attggcattg cgattccaca cggctgggcg acagagtcac	480
15	caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat	540
	ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcacccccctg	600
	gggggtatddd gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact	660
20	tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca	720
	ggtcaaggag gtcacgacga atgacggcgt cacaaccatc gctaataacc ttaccagcac	780
	ggttcaggtc ttttcggact cggaatatca actgccgtac gtccctcggct ccgcgcacca	840
25	gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtacg gatacctgac	900
	tctgaacaat ggcagccaat cggtaggccc ttccctcttc tactgcctgg agtactttcc	960
	ttctcagatg ctgagaacgg gcaacaactt caccttttagc tacaccttcg aggacgtgcc	1020
30	tttccacagc agctacgcgc acagccagag tctgggcccgg ctgatgaatc ccctcatcga	1080
	ccagtacctg tactacttgg ccagaacaca gagcaacgca ggagggtactg ctggcaatcg	1140
	ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct	1200
35	gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag	1260
	caactttgcc tggactggtg ccacaaaata ccattttaat ggaagaaatt cattgggttaa	1320
	tcccgggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttcttcc cttcgagcgg	1380
40	agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat	1440
	gacaaatgaa gaagaaattc gtccctacca cccggtagct accgaggaat acgggattgt	1500
	aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg	1560
45	agccttacct ggcatggtct ggcagaaccg ggacgtgtac ctgcaaggct ccatttgggc	1620
	caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact	1680
	gaaacacccg cctccccaga tccatgatcaa aaacacaccg gtacctgcta atcctccaga	1740
50	agtgtttact cctgccaaagt ttgcttcctt catcacgcag tacagcaccg ggcaagtcag	1800
	cgttgagatc gaatgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca	1860
	gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt	1920
55	ttactctgag cct	1933

EP 1 310 571 B1

<211> 1933

<212> DNA

<213> new AAV serotype, clone 223.6

5

<400> 52

	caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc	60
10	cgacgccgag tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg	120
	agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc	180
	taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg	240
15	caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga	300
	gtcagtcccc gacctcaac caatcggaga accaccagca ggcccctctg gtctgggatc	360
	tggtacaatg gctgcaggcg gtggcgaccc aatggctgac aatagcgagg gcgccgacgg	420
20	agtgggtaat gcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcac	480
	caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaa	540
	ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcacccctg	600
25	ggggtatttt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact	660
	tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca	720
	ggtcaaggag gtcacgacga atgacggtgt cacaaccatc gctaataacc ttaccagcac	780
30	ggttcaggtc ttttcggact cggaatatca actgccgtac gtccctcggct ccgcgcacca	840
	gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtagc gatacctgac	900
	tctgaacaat ggcagccaat cggtaggcgg ttcctccttc tactgcctgg agtactttcc	960
35	ttctcagatg ctgagaacgg gcaacaactt cacctttagc tacaccttcg aggacgtgcc	1020
	tttccacagc agctacgcgc acagccagag tctggaccgg ctgatgaatc cctcatcga	1080
	ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtagtg ctggcaatcg	1140
40	ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct	1200
	gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag	1260
	caactttgcc tggactggtg ccacaaaata ccattttaat ggaagaaatt cattgggttaa	1320
45	tcccgggtgc gccatggcaa cccacaagga cgacgaggaa cgcttcttcc cttcgagcgg	1380
	agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat	1440
	gacaaatgaa gaagaaattc gtcctacca cccggtagct accgaggaat acgggattgt	1500
50	aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg	1560
	agccttacct ggcattggtc ggcagaaccg ggacgtgtac ctgcaaggtc ccatttgggc	1620
	caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact	1680
55	gaaacacccg cctcccaga tcctgatcaa aaacacaccg gtacctgcta atcctcaga	1740

EP 1 310 571 B1

	agtgtttact cctgccaagc ttgcttcctt catcacgcag tacagcaccg ggcaagtcag	1800
	cgttgagatc gagtgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca	1860
5	gtaçacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccaggggtgt	1920
	ttactctgag cct	1933
10	<210> 53 <211> 1933 <212> DNA <213> new AAV serotype, clone 223.7	
15	<400> 53	
	caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc	60
	cgacgccgag tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg	120
20	agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc	180
	taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg	240
	caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga	300
25	gtcagtcccc gaccctcaac caatcggaga accaccagca ggccccctctg gtctggggtc	360
	tggtacaatg gctgcaggcg gtggcgccacc aatggctgac aataacgagg gcgccgacgg	420
	agtgggtaat gcctcaggaa attggcattg cgattccaca tggtcgggcg acagagtcac	480
30	caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat	540
	ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggtaca gcacccctctg	600
	gggggtatattt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact	660
35	tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca	720
	ggtcaaggag gtcacgacga atgacggcgt cacaaccatc gctaataacc ttaccagcac	780
	ggttcagggtc ttttcggacc cggaatatca actgccgtac gtctcgggt ccgcgcacca	840
40	gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtagc gatacctgac	900
	tctgaacaat ggcagccaat cggtaggccg ttctctcttc tactgcctgg agtactttcc	960
	ttctcagatg ctgagaacgg gcaacaactt caccttttagc tacaccttcg aggacgtgcc	1020
45	tttccacagc agctacgagc acagccagag tctggaccgg ctgatgaatc ccctcatcga	1080
	ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg	1140
	ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct	1200
50	gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag	1260
	caactttgcc tggactggtg ccacaaaata ccattttaat ggaagaaatt cattgggttaa	1320
	tcccgggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttcttcc cttcgagcgg	1380
55	agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat	1440
	gacaaatgaa gaagaaattc gtcctaccaa cccggtagct accgaggaat acgggattgt	1500

EP 1 310 571 B1

	aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg	1560
	agccttacct ggcattggtct ggcagaaccg ggacgtgtac ctgcaaggtc ccatttgggc	1620
5	caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact	1680
	gaaacacccg cctccccaga tcctgatcaa aaacacaccg gtacctgcta atcctccaga	1740
	agtgtttact cctgccaaga ttgcttcctt catcacgcag tacagcaccg ggcaagtcag	1800
10	cgttgagatc gagtgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca	1860
	gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt	1920
	ttactctgag cct	1933
15		
	<210> 54	
	<211> 3123	
	<212> DNA	
	<213> new AAV serotype, clone A3.4	
20		
	<400> 54	
	gaattcgccc tttctacggc tgcgtcaact ggaccaatga aaactttccc ttcaacgatt	60
25	gcgtcgacaa gatggtgatc tgggtgggagg agggaaagat gaccgccaag gtcgtggaat	120
	ctgccaaagc cattctgggt ggaagcaagg ttcgtgtgga ccagaaatgc aagtcttcgg	180
	cccagatcga cccgactccg gtgattgtca cctctaacac caacatgtgc gccgtgattg	240
30	acggaaaactc gaccaccttc gagcaccagc agccgttgca agaccggatg ttcaaatttg	300
	aacttaccgg ccgtttggat catgactttg ggaaggtcac caagcaggaa gtcaaagact	360
	ttttccgggtg ggctcaagat cacgtgactg aggtggagca tgagttctac gtcaaaaagg	420
35	gtggagccaa gaaaaggccc gccccgatg atgtatatat aaatgagccc aagcgggcgc	480
	gcgagtcagt tgcgcagcca tcgacgtcag acgcggaagc ttcgataaac tacgcgggca	540
	ggtacaaaaa caaatgttct cgtcacgtgg gcatgaatct gatgctgttt ccctgtcgac	600
40	aatgcgaaag aatgaatcag aattcaaata tctgcttcac acacgggcaa aaagactgtt	660
	tggaatgctt tcccgtgtca gaatctcaac ccgtttctgt cgtcagaaaa acgtatcaga	720
	aactttgtta cattcatcat atcatgggaa aagaaccaga cgccctgact gcctgcgacc	780
45	tggtaaatgt ggacttggat gactgtatct ctgagcaata aatgacttaa atcaggatg	840
	gctgctgacg gttatcttcc agattggctc gaggacactc tctctgaagg aatcagacag	900
	tggtggaagc tcaaacctgg cccaccaccg ccgaaacctt accaacaaca ccgggacgac	960
50	agtaggggtc ttgtgcttcc tgggtacaag tacctcggac ctttcaacgg actcgacaaa	1020
	ggagagccgg tcaacgaggc agacgcgcgc gccctcgagc acgacaaagc ctacgaccac	1080
	cagctcaagc aaggggacaa cccgtacctc aaatacaacc acgcggacgc tgaatttcag	1140
55	gagcgtcttc aagaagatac gtctttcggg ggcaacctcg ggcgagcagt cttccaggcc	1200
	aaaaagaggg tactcgagcc tcttggctctg gttgaggaag ctgttaagac ggctcctgga	1260

EP 1 310 571 B1

	aaaaagagac ctatagagca gtctcctgca gaaccggact cttcctcggg catcggcgaa	1320
	tcaggccagc agcccgctaa gaaaagactc aattttggtc agactggcga cacagagtca	1380
5	gtccagacc ctcaaccaat cggagaaccc cccgcagccc cctctggtgt gggatctaata	1440
	acaatggctt caggcgggtg ggcaccaatg gcagacgata acgaaggcgc cgacggagt	1500
	ggtaattcct cgggaaattg gcattgcgat tccacatgga tgggcgacag agttatcacc	1560
10	accagcacaa gaacctgggc cctccccacc tacaataatc acctctacaa gcaaactctcc	1620
	agcgaatcgg gagccaccaa cgacaaccac tacttcggct acagcacccc ctgggggtat	1680
	tttgacttta acagattcca ctgtcacttc tcaccacgtg actggcagcg actcatcaac	1740
15	aacaactggg gatttagacc caagaaactc aatttcaagc tcttcaacat ccaagtcaag	1800
	gaggtcacgc agaattgatg aaccacgacc atcgccaata accttaccag cacgggtgcag	1860
	gtcttcacag actctgagta ccagctgccc tacgtcctcg gttcggctca ccagggctgc	1920
20	cttcgccgt tcccagcaga cgtcttcattg attcctcagt acggctactt gactctgaac	1980
	aatggcagcc aagcggtagg acgttcttca ttctactgtc tagagtattt tccctctcag	2040
	atgctgagga cgggaaacaa cttcaccttc agctacactt ttgaagacgt gcctttccac	2100
25	agcagctacg cgcacagcca gagtctggat cggctgatga atcctctcat tgaccagtac	2160
	ctgtattacc tgagcaaaac tcagggtaca agtggaaacaa cgcagcaatc gagactgcag	2220
	ttcagccaag ctgggcctag ctccatggct cagcaggcca aaaactggct accgggaccc	2280
30	agctaccgac agcagcgaat gtctaagacg gctaattgaca acaacaacag tgaatttgct	2340
	tggactgcag ccaccaata ttacctgaat ggaagaaatt ctctggtcaa tcccgggccc	2400
	ccaatggcca gtcacaagga cgatgaggaa aagtatttcc ccatgcacgg aaatctcatc	2460
35	tttggaaaac aaggcacagg aactaccaat gtggacattg aatcagtgct tattacagac	2520
	gaagaagaaa tcagaacaac taatcctgtg gctacagaac aatacggaca ggttgccacc	2580
	aaccatcaga gtcaggacac cacagcttcc tatggaagtg tggacagcca gggaatctta	2640
40	cctggaatgg tgtggcagga ccgcgatgtc tatcttcaag gtcccatttg ggccaaaact	2700
	cctcacacgg acggacactt tcatccttct ccgctcatgg gaggttttg actgaaacac	2760
	cctcctcccc agatcctgat caaaaacaca cctgtgccag cgaatccgc gaccactttc	2820
45	actcctggaa agtttgcttc gttcattacc cagtattcca ccggacaggt cagcgtggaa	2880
	atagagtggg agctgcagaa agaaaacagc aaacgctgga acccagaaat tcagtacacc	2940
	tccaactaca acaagtcggt gaatgtggag ttaccgtgg acgcaaacgg tgtttattct	3000
50	gaacccccgc ctattggcac tcgttacctt acccggaact tgtaatttcc tgtaaatgaa	3060
	taaaccgatt tatgcgtttc agttgaactt tgggtctctgc gaagggcgaa ttcgcggccg	3120
55	cta	3123

<210> 55

<211> 3113

EP 1 310 571 B1

<212> DNA

<213> new AAV serotype, clone A3.5

<400> 55

5

```

gaattcgccc tttctacggc tgcgtcaact ggaccaatga aaactttccc ttcaacgatt      60
gcgtcgacaa gatgggtgatc tgggtgggagg agggaaagat gaccgccaag gtcgtggaat      120
ctgccaaagc cattctgggt ggaagcaagg ttcgtgtgga ccagaaatgc aagtcttcgg      180
cccagatcga cccgactccg gtgattgtca cctctaacac caacatgtgc gccgtgattg      240
acggaaactc gaccaccttc gagcaccagc agccgttgca agaccggatg ttcaaatttg      300
aacttacccg ccgtttggat catgactttg ggaagggtcac caagcaggaa gtcaaagact      360
ttttccgggtg ggctcaagat cacgtgactg aggtggagca tgagttctac gtcaaaaagg      420
gtggagccaa gaaaaggccc gccccgatg atgtatatat aaatgagccc aagcgggcgc      480
gcgagtcagt tgcgcagcca tcgacgtcag acgcggaagc ttcgataaac tacgcggaca      540
ggtacaaaaa caaatgttct cgtcacgtgg gcatgaatct gatgctgttt ccctgtcgac      600
aatgcgaaag aatgaatcag aattcaaata tctgcttcac acacgggcaa aaagactgtt      660
tggaatgctt tcccgtgtca gaatctcaac ccgttcctgt cgtcagaaaa acgtatcaga      720
aactttgtta cattcatcat atcatgggaa aagtaccaga cgcctgcaact gcctgcgacc      780
tggtaaatgt ggacttggat gactgtattt ctgagcaata aatgacttaa atcaggtatg      840
gctgctgacg gttatcttcc agattggctc gaggacactc tctctgaagg aatcagacag      900
tggtggaagc tcaaacctgg cccaccaccg ccgaaacctt accaacaaca ccgggacgac      960
agtaggggtc ttgtgcttcc tgggtacaag tacctcggac ctttcaacgg actcgacaaa     1020
ggagagccgg tcaacgaggc agacgccgcg gcctcagagc acgacaaagc ctacgaccac     1080
cagctcaagc aaggggacaa cccgtacctc aaatacaacc acgcggacgc tgaatttcag     1140
gagcgtcttc aagaagatac gtctttcggg ggcaacctcg ggcgagcagt cttccaggcc     1200
aaaaagaggg tactcgagcc tcttgggtctg gttgaggaag ctgttaagac ggctcctgga     1260
aaaaagagac ctatagagca gtctcctgca gaaccggact cttcctcggg catcggcaaa     1320
tcaggccagc agcccgctaa gaaaagactc aattttggtc agactggcga cacagagtca     1380
gtcccagacc ctcaaccaat cggagaacct ccgcagccc cctctggtgt gggatctaata     1440
acaatggctt caggcgggtg ggcaccaatg gcagacaata acgaaggcgc cgacggagtg     1500
ggtaattcct cgggaaattg gcattgcatg tccacatgga tgggagacag agttatcacc     1560
accagcacia gaacctgggc cctccccacc tacaataatc acctctacaa gcaaattctc     1620
agcgaatcgg gagccaccaa cgacaaccac tacttcggct acagcaccac ctgggggtat     1680
tttgacttta acagattcca ctgtcacttc tcaccacgtg actggcagcg actcatcaat     1740

```

55

EP 1 310 571 B1

5
10
15
20
25
30
35
40

aacaactggg	gatttagacc	caagaaactc	aatttcaagc	tcttcaacat	ccaagtcaag	1800
gaggtcacgc	agaatgatgg	aaccacgacc	atcgccaata	accttaccag	cacggtgcag	1860
gtcttcacag	actctgagta	ccagctgccc	tacgtcctcg	gttcggctca	ccagggctgc	1920
cttccgccgt	ttccagcaga	cgtcttcattg	attcctcagt	acggctactt	gactctgaac	1980
aatggcagcc	aagcggtagg	acgttcttca	ttctactgtc	tagagtattt	tccctctcag	2040
atgctgagga	cgggaaacaa	cttcaccttc	agctacactt	ttgaagacgt	gcctttccac	2100
agcagctacg	cgcacagcca	gagtcctggat	cggctgatga	atcctctcat	tgaccagtac	2160
ctgtattacc	tgagcaaaac	tcaggggtaca	agtggaacaa	cgcagcaatc	gagactgcag	2220
ttcaaccaag	ctgggcctag	ctccatggct	cagcaggcca	aaaactgggt	accgggaccc	2280
agctaccgac	agcagcgaat	gtctaagacg	gctaatagaca	acaacaacag	tgaatttgct	2340
tggactgcag	ccaccaata	ttacccgaat	ggaagaaatt	ctctggtcaa	ttccggggccc	2400
ccaatggcca	gtcacaagga	cgatgaggaa	aagtatttcc	ccatgcacgg	aaatctcatc	2460
tttgaaaaac	aaggcacagg	aactaccaat	gtggacattg	aatcagtgct	tattacagac	2520
gaagaagaaa	tcagaacgac	taatcctgtg	gctacagaac	aatacggaca	ggttgccacc	2580
aaccgtcaga	gtcagaacac	cacagcttcc	tatggaagtg	tggacagcca	gggaatctta	2640
cctggaatgg	tgtggcagga	ccgcgatgtc	tatcttcaag	gtcccatttg	ggccaaaact	2700
cctcacacgg	acggacactt	tcattccttct	ccgctcatgg	gaggctttgg	actgaaacac	2760
cctcctcccc	agatcctgat	caaaaacaca	cctgtgccag	cgaatcccg	gaccactttc	2820
actcctggaa	agtttgcttc	gttcattacc	cagtattcca	ccggacaggt	cagcgtggaa	2880
atagagtggg	agctgcagaa	agaaaacagc	aaacgctgga	accgggaaat	tcagtacacc	2940
tccaactaca	acaagtcggt	gaatgtggag	tttaccgtgg	acgcaaacgg	tgttttattct	3000
gaaccccgcc	ctattggcac	tcgttacctt	acccggaact	tgtaatttcc	tgttaatgaa	3060
taaaccgatt	tatgcgtttc	agttgaactt	tggctctctgc	gaagggcgaa	ttc	3113

<210> 56

<211> 3122

<212> DNA

<213> new AAV serotype, clone A3.7

<400> 56

EP 1 310 571 B1

	agcggccgcg aattcgccct ttctacggct gcgtcaactg gaccaatgaa aactttccct	60
	tcaacgattg cgtcgacaag atggtgatct ggtgggagga gggaaagatg accgccaagg	120
5	tcgtggaatc tgccaaagcc attctgggtg gaagcaaggt tcgtgtggac cagaaatgca	180
	ggtcttcggc ccagatcgac ccgactccgg tgattgtcac ctctaacacc aacatgtgcg	240
	ccgtgattga cggaaactcg accaccttcg agcaccagca gccgttgcaa gaccggatgt	300
10	tcaaatttga acttaccgcg cgtttggatc atgactttgg gaaggtcacc aagcaggaag	360

15

20

25

30

35

40

45

50

55

EP 1 310 571 B1

	tcaaagactt tttccggtgg gctcaagatc acgtgactga ggtggagcat gagttctacg	420
	tcaaaaagggt tggagccaag aaaaggcccg ccccgatga tgtatatata aatgagccca	480
5	agcgggcgcg cgagtcagtt gcgcagccat cgacgtcaga cgcggaagct tcgataaact	540
	acgcggacag gtaccaaaac aaatgtttctc gtcacgtggg catgaatctg atgctgtttc	600
10	cctgtcgaca atgcgaaaga atgaatcaga attcaaatat ctgcttcaca cacgggcaaa	660
	aagactgttt ggaatgcttt cccgtgtcag aatctcaacc cgtttctgtc gtcagaaaaa	720
	cgtatcagaa actttgttac attcatcata tcatgggaaa agtaccagac gcctgcactg	780
15	cctgcgacct ggtaaatgtg gacttggatg actgtatttc tgagcaataa atgacttaaa	840
	tcagggtatgg ctgctgacgg ttatcttcca gattggctcg aggacactct ctctgaagga	900
	atcagacagt ggtggaagct caaacctggc ccaccaccgc cgaaacctaa ccaacaacac	960
20	cgggacgaca gtaggggtct tgtgtcttcct gggtacaagt acctcggacc cttcaacgga	1020
	ctcgacaaag gagagccggt caacgaggca gacgccgcgg ccctcgagca cgacaaagcc	1080
	tacgaccacc agctcaagca aggggacaac ccgtacctca aatacaacca cgcggacgct	1140
25	gaatttcagg agcgtcttca agaagatacg tctttcgggg gcaacctcgg gcgagcagtc	1200
	ttccaggcca aaaagaggggt actcgagcct cttgggtctgg ttgaggaagc tgttaagacg	1260
	gctcctggaa aaaagagacc tatagagcag tctcctgcag aaccggactc ttcctcgggc	1320
30	atcggcaaat caggccagca gcccgctaag aaaagactca attttggta gactggcgac	1380
	acagagtcag tcccagacc tcaaccaatc ggagaacccc ccgcagcccc ctctggtgtg	1440
	ggatctaata caatggcttc aggcgggtggg gcaccaatgg cagacaataa cgaaggcgcc	1500
35	gacggagtgg gtaattcctc gggaaattgg cattgcgatt ccacatggat gggcgacaga	1560
	gttatcacca ccagcacaag aacctgggcc ctccccacct acaataatcg cctctacaag	1620
	caaatctcca gcgaatcggg agccaccaac gacaaccact acttcggcta cagcaccccc	1680
40	tgggggtatt ttgactttaa cagattccac tgtcacttct caccacgtga ctggcagcga	1740
	ctcatcaaca acaactgggg atttagacc aagaaactca atttcaagct cttcaacatc	1800
	caagtcaagg aggtcacgca gaatgatgga accacgacca tcgccataa ccttaccagc	1860
45	acggtgcagg tcttcacaga ctctgagtac cagctgccct acgtcctcgg ttcggtcac	1920
	cagggctgcc ttcgcgcgtt ccagcagac gtcttcatga ttctcagta cggctacttg	1980
	actctgaaca atggcagcca agcggtagga cgttcttcat tctactgtct agagtatttt	2040
50	ccctctcaga tgctgaggac gggaaacaac ttcaccttca gctacacttt tgaagacgtg	2100
	cctttccaca gcagctacgc gcacagccag agtctggatc ggctgatgaa tcctctcatt	2160
	gaccagtacc tgtattacct gagcaaaact caggggtacaa gtggaacaac gcagcaatcg	2220
55	agactgcagt tcagccaagc tgggcctagc tccatggctc agcaggccaa aaactggcta	2280

EP 1 310 571 B1

	ccgggaccca gctaccgaca gcagcgaatg tctaagacgg ctaatgacaa caacaacagt	2340
	gaatttgctt ggactgcagc caccaaatac tacctgaatg gaagaaattc tctgggtcaat	2400
5	cccgggcccc caatggccag tcacaaggac gatgaggaaa agtatttccc catgcacgga	2460
	aatctcatct ttggaaaaca aggcacagga actaccaatg tggacattga atcagtgtctt	2520
	attacagacg aagaagaaat cagaacaact aatcctgtgg ctacagaaca atacggacag	2580
10	gttgccacca accatcagag tcagaacacc acagcttcct atggaagtgt ggacagccag	2640
	ggaatcttac ctggaatggt gtggcaggac cgcgatgtct atcttcaagg tcccatttgg	2700
	gccccaaactc ctcacacgga cggacacttt catccttctc cgctcatggg aggcctttgga	2760
15	ctgaaacacc ctcctcccca gatcctgatc aaaaacacac ctgtgccagc gaatcccgcg	2820
	accactttca ctcctggaaa gtttgcttcg ttcattaccc agtattccac cggacaggtc	2880
	agcgtggaaa tagagtggga gctgcagaaa gaaaacagca aacgctggaa cccagaaatt	2940
20	cagtacacct ccaactacaa caagtcggtg aatgtggagt ttaccgtgga cgcaaacggt	3000
	gtttattctg ,aaccocgccc tattggcact cgttacctta cccggaactt gtaatttcct	3060
	gttaatgaat aaaccgattt atgcgtttca gttgaacttt ggtctctgcg aagggcgaat	3120
25	tc	3122

30	<210> 57
	<211> 3123
	<212> DNA
	<213> new AAV serotype, clone A3.3
35	<400> 57

40

45

50

55

EP 1 310 571 B1

	gaattcgccc tttctacggc tgcgtcaact ggaccaatga aaactttccc ttcaacgatt	60
	gcgtcgacaa gatggtgatc tgggtgggagg agggaaagat gaccgccaag gtcgtggaat	120
5	ctgccaaagc cattctgggt ggaggcaagg ttcgtgtgga ccagaaatgc aagtcttcgg	180
	cccagatcga cccgactccg gtgattgtca cctctaacac caacatgtgc gccgtgattg	240
	acggaaaactc gaccaccttc gagcaccagc agccgttgca agaccggatg ttcaaatttg	300
10	aacttaccgg ccgtttggat catgactttg ggaaggtcac caagcaggaa gtcaaagact	360
	ttttccggtg ggctcaagat cacgtgactg aggtggagca tgagttctac gtcaaaaagg	420
	gtggagccaa gaaaaggccc gccccgatg atgtatatat aaatgagccc aagcgggagc	480
15	gcgagtcagt tgcgcagcca tcgacgtcag acgcggaagc ttcgataaac tacgcggaca	540
	ggtaccaaaa caaatgttct cgtcacgtgg gcatgaatct gatgctgttt ccctgtcgac	600
	aatgcgaaag aatgaatcag aattcaaata tctgcttcac acacgggcaa aaagactgtt.	660
20	tggaatgctt tcccgtgtca gaatctcaac ccgtttctgt cgtcagaaaa acgtatcaga	720
	aactttgtta cattcatcat atcatgggaa aagtaccaga cgcctgcact gcctgagacc	780
	tggtaaatgt ggacttggat gactgtattt ctgagcaata aatgacttaa atcaggtatg	840
25		
30		
35		
40		
45		
50		
55		

EP 1 310 571 B1

							900
							960
5							1020
							1080
							1140
10							1200
							1260
							1320
15							1380
							1440
							1500
20							1560
							1620
							1680
25							1740
							1800
							1860
30							1920
							1980
							2040
35							2100
							2160
							2220
40							2280
							2340
							2400
45							2460
							2520
							2580
50							2640
							2700
55							2760

EP 1 310 571 B1

	cctcctcccc agatcctgat caaaaacaca cctgtgccag cgaatccgc gaccactttc	2820
	actcctggaa agtttgcttc gttcattacc cagtattcca cctgacaggt cagcgtggaa	2880
5	atagagtggg agctgcagaa agaaaacagc aaacgctgga acccagaaat tcagtacacc	2940
	tccaactaca acaagtcggt gaatgtggag ttaccgtgg acgcaaacgg tgtttattct	3000
	gaaccccgcc ctattggcac tcgttacctt acccggaact tgtaatttcc tgttaatgaa	3060
10	taagccgatt tatgcgtttc agttgaactt tggctctctc gaagggcgaa ttcgtttaaa	3120
	cct	3123

15 <210> 58
 <211> 2969
 <212> DNA
 <213> new AAV serotype, clone 42.12

20 <400> 58

25

30

35

40

45

50

55

EP 1 310 571 B1

	gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt	60
	gcgctcgacaa gatggtgac tgggtgggagg agggcaagat gacggccaag gtcgtggagt	120
5	ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg	180
	cccagatcga ccccaacccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg	240
	acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg	300
10	aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcaaagagt	360
	tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg	420
	gtggagccaa caagagaccc gccccgatg acgcggataa aagcgagccc aagcgggcct	480
15	gccccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg	540
	acaggtagca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca	600
	agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact	660
20	gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc	720
	ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct	780
	gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca	840
25	ggtatggctg ccgatgggta tcttccagat tggctcgagg acaacctctc tgagggcatc	900
	cgcgagtggg gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag	960
	gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc	1020
30	gacaagggag agccgggtcaa cgaggcagac gccgcggccc tcgagcacga caaggcctac	1080
	gacaagcagc tcgagcaggg ggacaacccg tacctcaagt acaaccacgc cgacgccgag	1140
	tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggag agcagtcttc	1200
35	caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct	1260
	cctggaaaga agagaccggt agagccatca cccagcgtt ctccagactc ctctacgggc	1320

40

45

50

55

EP 1 310 571 B1

atcggcaaga caggccagca gcccgcgaaa aagagactca acttttgggca gactggcgac 1380
 tcagagtcag tgccccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctgggtctg 1440
 5 ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500
 gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560
 gtcatcacca ccagcaccgg aacctggggc ctccccacct acaacaacca cctctacaag 1620
 10 caaatctcca acgggacatc gggaggaagc accaacgaca acacctactt cggtctacagc 1680
 accccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740
 cagcgactca tcaacaacaa ctgggggattc cgggccaaga gactcaactt caagctcttc 1800
 15 aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860
 accagcacga ttcaggctct tacggactcg gaataccagc tcccgtaagt cctcggctct 1920
 gcgcaccagg gctgcctgcc tccgttcccc gcggacgtct tcatgattcc tcagtacggg 1980
 20 tacctgactc tgaacaacgg cagtcaggcc gtgggcccgtt cctccttcta ctgcctggag 2040
 tactttcctt ctcaaatgct gagaacgggc aacaactttg agttcagcta ccagtttgag 2100
 gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gacgaacccc 2160
 25 ctcatcgacc agtacctgta ctacctggcc cggaccaga gactacggg gtccacaagg 2220
 gggctgcagt tccatcaggc tggggccaac accatggccg agcaatcaa gaactggctg 2280
 cccggaccct gttatcggca gcagagactg tcaaaaaaca tagacagcaa caacaacagt 2340
 30 aactttgcct ggaccggggc cactaaatac catctgaatg gtagaaattc attaaccaac 2400
 ccgggcgtag ccatggccac caacaaggac gacgaggacc agttctttcc catcaacgga 2460
 gtgctggttt ttggcaaac gggggctgcc aacaagacaa cgctggaaaa cgtgctaattg 2520
 35 accagcgagg aggagatcaa aaccaccaat cccgtggcta cagaagaata cgggtgtggtc 2580
 tccagcaacc tgcaatcgtc tacggccgga cccagacac agactgtcaa cagccagggg 2640
 gctctgcccg gcatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctggggc 2700
 40 aaaattcctc acacggacgg caactttcac cgtctcccc tgatgggcgg atttggactc 2760
 aaacaccggc ctctcaaat tctcatcaag tatacttcca actactacaa atctacaaat 2820
 gtggactttg ctgtcaatac tgagggtact tattcagagc ctgccccat tggcaccggt 2880
 45 tacctcaccg gtaacctgta attgcctggt aatcaataaa ccggttaatt cgtttcagtt 2940
 gaactttggt ctctgcgaag ggcgaattc 2969

50 <210> 59
 <211> 3129
 <212> DNA
 <213> new AAV serotype, clone 44.2
 55 <400> 59

EP 1 310 571 B1

gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

5

10

15

20

25

30

35

40

45

50

55

EP 1 310 571 B1

	gcgtcgacaa gatggtgatc tgggtgggagg agggcaagat gacggccaag gtcgtggagt	120
	ccgccaaggc cattctcggc ggcagcaaag tgcgcgtgga ccaaaagtgc aagtcgtccg	180
5	cccagatcga ccccaacccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg	240
	acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaagtttg	300
10	aactcaccgg ccgtctggag cacgactttg gcaagggtgac aaagcaggaa gtcagagagt	360
	tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca cgagttctac gtcagaaagg	420
	gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct	480
15	gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg	540
	acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca	600
	aaacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact	660
20	gttcagaatg tttccccggc gtgtcagaat ctcaaccggc cgtcagaaaa aagacgtatc	720
	ggaaactctg tgcgattcat catctgctgg gggcgggcac ccgagattgc ttgctcggcc	780
	tgcgatctgg tcaacgtgga cctagatgac tgtgtttctg agcaataaat gacttaaacc	840
25	aggtatggct gccgatggtt atcttccaga ttggtctgag gacaacctct ctgagggcat	900
	tcgcgagtgg tgggacttga aacctggagc cccgaaacct aaagccaacc agcaaaagca	960
	ggacgacggc cgggggtctgg tgcttcctgg ctacaagtac ctcggaccct tcaacggact	1020
30	cgacaagggg gagcccgta acgcggcgga cgcagcggcc ctcgagcacg acaaggccta	1080
	cgaccagcag ctcaaagcgg gtgacaatcc gtacctgcgg tataaccacg ccgacgccga	1140
	gtttcaggag cgtctgcaag aagatacgtc ttttgggggc aacctcgggc gagcagtctt	1200
35	ccaggccaag aagcgggttc tcgaacctct cgggtctggtt gaggaaggcg ctaagacggc	1260
	tcctggaaaag aagagaccgg tagagccatc accccagcgt tctccagact cctctacggg	1320
	catcggcaag aaaggccagc agcccgcgaa aaagagactc aactttgggc agactggcga	1380
40	ctcagagtca gtgcccgaac ctcaaccaat cggagaacct cccgcaggcc cctctggtct	1440
	gggatctggt acaatggctg caggcgggtg cgctccaatg gcagacaata acgaaggcgc	1500
	cgacggagtg ggtagttcct caggaaattg gcattgcgat tccacatggc tgggcgacag	1560
45	agtcattacc accagcacc gaacctgggc cctccccacc tacaacaacc acctctacaa	1620
	gcaaatctcc aacgggactt cgggaggaag caccaacgac aacacctact tcggctacag	1680
	caccccctgg gggtattttg actttaacag attccactgc cacttctcac cacgtgactg	1740
50	gcagcgactc atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt	1800
	caacatccag gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct	1860
	taccagcacg attcaggtct ttacggactc ggaataccag ctcccgtacg tcctcggctc	1920
55	tgcgcaccag ggctgcctgc ctccgttccc ggcggacgtc ttcattgattc ctcagtacgg	1980

EP 1 310 571 B1

	gtacctgact ctgaacaatg gcagtcaggc cgtgggccgt tcctccttct actgcctgga	2040
	gtacttttcct tctcaaatgc tgagaacggg caacaacttt gagttcagct accagtttga	2100
5	ggacgtgcct tttcacagca gctacgcgca cagccaaagc ctggaccggc tgatgaaccc	2160
	cctcatcgac cagtacctgt actacctgtc tcggactcag tccacgggag gtaccgcagg	2220
	aactcagcag ttgctatttt ctcaggccgg gcctaataac atgtcggctc aggccaaaaa	2280
10	ctggctaccc gggccctgct accggcagca acgcgtctcc acgacactgt cgcaaaaataa	2340
	caacagcaac tttgcctgga ccggtgccac caagtatcat ctgaatggca gagactctct	2400
	ggtaaattccc ggtgtcgcta tggcaaccga caaggacgac gaagagcgat tttttccgtc	2460
15	cagcggagtc ttaatgtttg ggaaacaggg agctggaaaa gacaacgtgg actatagcag	2520
	cgttatgcta accagtgagg aagaaattaa aaccaccaac ccagtggcca cagaacagta	2580
	cggcgtggtg gccgataacc tgcaacagca aaacgccgct cctattgtag gggccgtcaa	2640
20	cagtcaagga gccttacctg gcatgggtctg gcagaaccgg gacgtgtacc tgcagggtcc	2700
	tatctgggcc aagattcctc acacggacgg aaactttcat ccctcgccgc tgatgggagg	2760
	ctttggactg aaacacccgc ctctcagat cctgattaag aatacacctg ttcccgcgga	2820
25	tcctccaact accttcagtc aagctaagct ggcgtcgttc atcacgcagt acagcaccgg	2880
	acaggtcagc gtggaaattg aatgggagct gcagaaagaa aacagcaaac gctggaaccc	2940
	agagattcaa tacacttcca actactacaa atctacaaat gtggactttg ctgttaacac	3000
30	agatggcact tattctgagc ctgcgcccat cggcaccggt tacctcaccg gtaatctgta	3060
	attgcttggt aatcaataaa ccggttgatt cgtttcagtt gaactttggg ctctgcgaag	3120
35	ggcgaattc	3129

<210> 60

<211> 733

<212> PRT

<213> capsid protein of AAV serotype, clone C1VP1

<400> 60

EP 1 310 571 B1

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

5 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

10 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

15

20

25

30

35

40

45

50

55

EP 1 310 571 B1

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 5
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 10
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 15
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
 145 150 155 160
 20
 Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
 165 170 175
 25
 Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
 180 185 190
 Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
 195 200 205
 30
 Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
 210 215 220
 35
 Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
 225 230 235 240
 Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
 245 250 255
 40
 Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
 260 265 270
 45
 Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
 275 280 285
 Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
 290 295 300
 50
 Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
 305 310 315 320
 55

EP 1 310 571 B1

5 Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
325 330 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
340 345 350

10 Leu Ser Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
355 360 365

Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
370 375 380

15 Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385 390 395 400

20 Asn Phe Glu Met Ala Tyr Asn Phe Gly Lys Val Pro Phe His Ser Met
405 410 415

Tyr Ala Tyr Ser Gln Ser Pro Asp Arg Leu Met Asn Pro Leu Leu Asp
420 425 430

25 Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
435 440 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
450 455 460

30 Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465 470 475 480

35 Arg Leu Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
485 490 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
500 505 510

40 Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
515 520 525

45 Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
530 535 540

50 Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545 550 555 560

Glu Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
565 570 575

55

EP 1 310 571 B1

5 Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
 580 585 590
 Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
 595 600 605
 10 Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
 610 615 620
 His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
 625 630 635 640
 15 Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala
 645 650 655
 20 Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
 660 665 670
 Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
 675 680 685
 25 Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Asn
 690 695 700
 30 Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
 705 710 715 720
 Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
 725 730

35

<210> 61

<211> 733

<212> PRT

40 <213> capsid protein of AAV serotype, clone C2VP1

<400> 61

45

50

55

EP 1 310 571 B1

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

5 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Leu
20 25 30

10 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe His Gly Leu Asp Lys Gly Glu Pro
50 55 60

15 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

20

25

30

35

40

45

50

55

EP 1 310 571 B1

5 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 10 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 15 Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
 145 150 155 160
 20 Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
 165 170 175
 Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
 180 185 190
 25 Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
 195 200 205
 30 Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
 210 215 220
 Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
 225 230 235 240
 35 Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
 245 250 255
 40 Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
 260 265 270
 Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
 275 280 285
 45 Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
 290 295 300
 50 Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
 305 310 315 320
 Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
 325 330 335
 55

EP 1 310 571 B1

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
 340 345 350
 5
 Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
 355 360 365
 10
 Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
 370 375 380
 Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
 385 390 395 400
 15
 Asn Phe Glu Met Ala Tyr Asn Phe Glu Lys Val Pro Phe His Ser Met
 405 410 415
 Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Leu Asp
 420 425 430
 20
 Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
 435 440 445
 25
 Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
 450 455 460
 Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
 465 470 475 480
 30
 Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
 485 490 495
 35
 Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
 500 505 510
 Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
 515 520 525
 40
 Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
 530 535 540
 45
 Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
 545 550 555 560
 Gly Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
 565 570 575
 50
 Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
 580 585 590
 55

EP 1 310 571 B1

Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
 595 600 605
 5
 Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
 610 615 620
 10
 His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
 625 630 635 640
 Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala
 645 650 655
 15
 Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
 660 665 670
 Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
 675 680 685
 20
 Ser Lys Arg Arg Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Asn
 690 695 700
 25
 Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
 705 710 715 720
 Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
 725 730
 30

<210> 62

<211> 733

35 <212> PRT

<213> capsid protein of AAV serotype, clone C5VP1@2

<400> 62

40

45

50

55

EP 1 310 571 B1

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

5 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

10 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Glu Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

15 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

20 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

25

30

35

40

45

50

55

EP 1 310 571 B1

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 5
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 10
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
 145 150 155 160
 15
 Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
 165 170 175
 20
 Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
 180 185 190
 Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
 195 200 205
 25
 Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
 210 215 220
 30
 Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
 225 230 235 240
 Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
 245 250 255
 35
 Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
 260 265 270
 40
 Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
 275 280 285
 Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
 290 295 300
 45
 Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
 305 310 315 320
 50
 Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
 325 330 335
 Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
 340 345 350
 55

EP 1 310 571 B1

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
 355 360 365
 5
 Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
 370 375 380
 10
 Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
 385 390 395 400
 Asn Phe Glu Thr Ala Tyr Asn Phe Glu Lys Val Pro Phe His Ser Met
 405 410 415
 15
 Tyr Ala His Ser Gln Ser Leu Asp Gly Leu Met Asn Pro Leu Leu Asp
 420 425 430
 20
 Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
 435 440 445
 Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
 450 455 460
 25
 Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
 465 470 475 480
 Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
 485 490 495
 30
 Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
 500 505 510
 35
 Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
 515 520 525
 Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
 530 535 540
 40
 Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
 545 550 555 560
 45
 Glu Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
 565 570 575
 Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
 580 585 590
 50
 Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
 595 600 605
 55

EP 1 310 571 B1

	Ile	Tyr	Tyr	Gln	Gly	Pro	Ile	Trp	Ala	Lys	Ile	Pro	His	Ala	Asp	Gly	
	610						615					620					
5	His	Phe	His	Pro	Ser	Pro	Leu	Ile	Gly	Gly	Phe	Gly	Leu	Lys	His	Pro	
	625					630					635					640	
	Pro	Pro	Gln	Ile	Phe	Ile	Lys	Asn	Thr	Pro	Val	Pro	Ala	Tyr	Pro	Ala	
10					645					650					655		
	Thr	Thr	Phe	Thr	Ala	Ala	Arg	Val	Asp	Ser	Phe	Ile	Thr	Gln	Tyr	Ser	
				660					665					670			
15	Thr	Gly	Gln	Val	Ala	Val	Gln	Ile	Glu	Trp	Glu	Ile	Glu	Lys	Glu	Arg	
			675					680					685				
	Ser	Lys	Arg	Trp	Asn	Pro	Glu	Val	Gln	Phe	Thr	Ser	Asn	Cys	Gly	Asn	
20		690					695					700					
	Gln	Ser	Ser	Met	Leu	Trp	Ala	Pro	Asp	Thr	Thr	Gly	Lys	Tyr	Thr	Glu	
	705					710					715					720	
25	Pro	Arg	Val	Ile	Gly	Ser	Arg	Tyr	Leu	Thr	Asn	His	Leu				
					725					730							

<210> 63

30 <211> 734

<212> PRT

<213> capsid protein of AAV serotype, clone AAV4VP1

<400> 63

35

40

45

50

55

EP 1 310 571 B1

Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1 5 10 15

5 Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
20 25 30

10 Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
50 55 60

15 Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65 70 75 80

20 Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
100 105 110

25

30

35

40

45

50

55

EP 1 310 571 B1

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
 115 120 125
 5
 Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
 130 135 140
 10
 Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
 145 150 155 160
 Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
 165 170 175
 15
 Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
 180 185 190
 20
 Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
 195 200 205
 Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
 210 215 220
 25
 Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
 225 230 235 240
 30
 Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
 245 250 255
 Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
 260 265 270
 35
 Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
 275 280 285
 40
 Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
 290 295 300
 Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
 305 310 315 320
 45
 Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
 325 330 335
 50
 Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
 340 345 350
 Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
 355 360 365
 55

EP 1 310 571 B1

Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
 370 375 380
 5
 Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
 385 390 395 400
 10
 Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
 405 410 415
 Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
 420 425 430
 15
 Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
 435 440 445
 20
 Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
 450 455 460
 Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
 465 470 475 480
 25
 Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
 485 490 495
 30
 Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
 500 505 510
 Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
 515 520 525
 35
 Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
 530 535 540
 40
 Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
 545 550 555 560
 Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
 565 570 575
 45
 Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
 580 585 590
 50
 Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
 595 600 605
 Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
 610 615 620
 55

EP 1 310 571 B1

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
 625 630 635 640
 5
 Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
 645 650 655
 10
 Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
 660 665 670
 Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
 675 680 685
 15
 Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
 690 695 700
 20
 Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
 705 710 715 720
 Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
 725 730
 25
 <210> 64
 <211> 736
 <212> PRT
 <213> capsid protein of AAV serotype, clone AAV1
 30
 <400> 64
 35
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 40
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 45
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 50
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 55
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125

EP 1 310 571 B1

5 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
 145 150 155 160
 10 Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
 180 185 190
 15 Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
 195 200 205
 20 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 25 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 30 Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
 260 265 270
 Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
 275 280 285
 35 His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
 290 295 300
 40 Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
 305 310 315 320
 Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
 325 330 335
 45 Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
 340 345 350
 50 Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
 355 360 365
 Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
 370 375 380

EP 1 310 571 B1

5
 Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
 385 390 395 400

10
 Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
 405 410 415

15
 Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
 420 425 430

20
 Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
 435 440 445

25
 Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
 450 455 460

30
 Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
 465 470 475 480

35
 Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
 485 490 495

40
 Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
 500 505 510

45
 Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
 515 520 525

50
 Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
 530 535 540

55
 Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
 545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
 565 570 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
 580 585 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
 595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
 610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
 625 630 635 640

EP 1 310 571 B1

5 Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
 645 650 655

 Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
 660 665 670

 10 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
 675 680 685

 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
 690 695 700

 15 Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
 705 710 715 720

 20 Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
 725 730 735

<210> 65

<211> 736

<212> PRT

<213> capsid protein of AAV serotype, clone AAV6VP1

<400> 65

EP 1 310 571 B1

	Met	Ala	Ala	Asp	Gly	Tyr	Leu	Pro	Asp	Trp	Leu	Glu	Asp	Asn	Leu	Ser
	1				5					10				15		
5	Glu	Gly	Ile	Arg	Glu	Trp	Trp	Asp	Leu	Lys	Pro	Gly	Ala	Pro	Lys	Pro
				20					25					30		
	Lys	Ala	Asn	Gln	Gln	Lys	Gln	Asp	Asp	Gly	Arg	Gly	Leu	Val	Leu	Pro
10			35					40					45			
	Gly	Tyr	Lys	Tyr	Leu	Gly	Pro	Phe	Asn	Gly	Leu	Asp	Lys	Gly	Glu	Pro
		50					55					60				
15	Val	Asn	Ala	Ala	Asp	Ala	Ala	Ala	Leu	Glu	His	Asp	Lys	Ala	Tyr	Asp
	65					70					75					80
	Gln	Gln	Leu	Lys	Ala	Gly	Asp	Asn	Pro	Tyr	Leu	Arg	Tyr	Asn	His	Ala
20					85					90					95	
	Asp	Ala	Glu	Phe	Gln	Glu	Arg	Leu	Gln	Glu	Asp	Thr	Ser	Phe	Gly	Gly
				100					105					110		
25	Asn	Leu	Gly	Arg	Ala	Val	Phe	Gln	Ala	Lys	Lys	Arg	Val	Leu	Glu	Pro
			115					120					125			
	Phe	Gly	Leu	Val	Glu	Glu	Gly	Ala	Lys	Thr	Ala	Pro	Gly	Lys	Lys	Arg
30		130					135					140				

EP 1 310 571 B1

5
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

10 Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
195 200 205

15 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
210 215 220

20 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

25 Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
260 265 270

30 Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
275 280 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
290 295 300

35 Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305 310 315 320

40 Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
325 330 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
340 345 350

45 Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
355 360 365

50 Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385 390 395 400

55

EP 1 310 571 B1

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
 405 410 415
 5
 Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
 420 425 430
 10
 Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
 435 440 445
 Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
 450 455 460
 15
 Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
 465 470 475 480
 20
 Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
 485 490 495
 Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
 500 505 510
 25
 Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
 515 520 525
 30
 Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
 530 535 540
 Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
 545 550 555 560
 35
 Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
 565 570 575
 40
 Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
 580 585 590
 Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
 595 600 605
 45
 Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
 610 615 620
 50
 Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
 625 630 635 640
 55
 Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
 645 650 655

EP 1 310 571 B1

5 Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
 660 665 670
 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
 675 680 685
 10 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
 690 695 700
 Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
 705 710 715 720
 15 Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
 725 730 735
 20 <210> 66
 <211> 735
 <212> PRT
 <213> capsid protein of AAV serotype, clone A3.3
 25 <400> 66
 30
 35
 40
 45
 50
 55

EP 1 310 571 B1

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

5 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

10 Lys Pro Asn Gln Gln His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

15 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

20 His Gln Leu Lys Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

25 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

30 Leu Gly Leu Val Glu Glu Ala Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

35

40

45

50

55

EP 1 310 571 B1

5 Pro Ile Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly
 145 150 155 160

 10 Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175

 15 Gly Asp Thr Glu Ser Val Pro Gly Pro Gln Pro Ile Gly Glu Pro Pro
 180 185 190

 20 Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
 195 200 205

 25 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220

 30 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240

 35 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255

 40 Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr
 260 265 270

 45 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285

 50 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300

 55 Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320

 60 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335

 65 Thr Ser Ala Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350

 70 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365

 75 Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380

 80 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400

EP 1 310 571 B1

5 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

10 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
435 440 445

Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Ser Gln
450 455 460

15 Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
465 470 475 480

20 Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn
485 490 495

Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Leu Asn Gly
500 505 510

25 Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Val Ala Ser His Lys Asp
515 520 525

30 Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
530 535 540

Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr
545 550 555 560

35 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

40 Gly Gln Val Ala Thr Asn His Gln Ser Gln Asn Thr Thr Ala Ser Tyr
580 585 590

Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
595 600 605

45 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Thr Pro His Thr
610 615 620

50 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

55

EP 1 310 571 B1

5 Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670

 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685

10 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700

 Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr
 705 710 715 720

15 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

20 <210> 67
 <211> 735
 <212> PRT
 <213> capsid protein of AAV serotype, clone A3.7

25 <400> 67

30

35

40

45

50

55

EP 1 310 571 B1

	Met	Ala	Ala	Asp	Gly	Tyr	Leu	Pro	Asp	Trp	Leu	Glu	Asp	Thr	Leu	Ser
	1				5					10					15	
5	Glu	Gly	Ile	Arg	Gln	Trp	Trp	Lys	Leu	Lys	Pro	Gly	Pro	Pro	Pro	Pro
				20					25					30		
	Lys	Pro	Asn	Gln	Gln	His	Arg	Asp	Asp	Ser	Arg	Gly	Leu	Val	Leu	Pro
10			35					40					45			
	Gly	Tyr	Lys	Tyr	Leu	Gly	Pro	Phe	Asn	Gly	Leu	Asp	Lys	Gly	Glu	Pro
		50					55					60				
15	Val	Asn	Glu	Ala	Asp	Ala	Ala	Ala	Leu	Glu	His	Asp	Lys	Ala	Tyr	Asp
	65					70					75					80
	His	Gln	Leu	Lys	Gln	Gly	Asp	Asn	Pro	Tyr	Leu	Lys	Tyr	Asn	His	Ala
20					85					90					95	
	Asp	Ala	Glu	Phe	Gln	Glu	Arg	Leu	Gln	Glu	Asp	Thr	Ser	Phe	Gly	Gly
				100					105					110		
25	Asn	Leu	Gly	Arg	Ala	Val	Phe	Gln	Ala	Lys	Lys	Arg	Val	Leu	Glu	Pro
			115					120					125			
	Leu	Gly	Leu	Val	Glu	Glu	Ala	Val	Lys	Thr	Ala	Pro	Gly	Lys	Lys	Arg
30		130					135					140				
	Pro	Ile	Glu	Gln	Ser	Pro	Ala	Glu	Pro	Asp	Ser	Ser	Ser	Gly	Ile	Gly
	145					150					155					160

EP 1 310 571 B1

5 Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
 180 185 190
 10 Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 15 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240
 20 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn Arg Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr
 260 265 270
 25 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 30 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 35 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 40 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 45 Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 50 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 55

EP 1 310 571 B1

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 5
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
 435 440 445
 Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 10
 Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
 465 470 475 480
 15
 Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn
 485 490 495
 Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Leu Asn Gly
 500 505 510
 20
 Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Met Ala Ser His Lys Asp
 515 520 525
 25
 Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr
 545 550 555 560
 30
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 35
 Gly Gln Val Ala Thr Asn His Gln Ser Gln Asn Thr Thr Ala Ser Tyr
 580 585 590
 Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 40
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Thr Pro His Thr
 610 615 620
 45
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 50
 Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 55

EP 1 310 571 B1

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 5
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 10
 Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr
 705 710 715 720
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735
 15
 <210> 68
 <211> 735
 <212> PRT
 <213> capsid protein of AAV serotype, clone A3.4
 20
 <400> 68
 25
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 30
 Lys Pro Asn Gln Gln His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 35
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 40
 His Gln Leu Lys Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 45
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 50
 Leu Gly Leu Val Glu Glu Ala Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Ile Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly
 145 150 155 160
 55
 Glu Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175

EP 1 310 571 B1

5 Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
195 200 205

10 Ala Pro Met Ala Asp Asp Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225 230 235 240

15 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

20 Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

25 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
290 295 300

30 Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

35 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
340 345 350

40 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380

45 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400

50 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

55

EP 1 310 571 B1

5 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
435 440 445

Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Ser Gln
450 455 460

10 Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
465 470 475 480

15 Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn
485 490 495

Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Leu Asn Gly
500 505 510

20 Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Met Ala Ser His Lys Asp
515 520 525

25 Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
530 535 540

Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr
545 550 555 560

30 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Gln Val Ala Thr Asn His Gln Ser Gln Asp Thr Thr Ala Ser Tyr
580 585 590

35 Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
595 600 605

40 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Thr Pro His Thr
610 615 620

45 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

50 Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

55 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

EP 1 310 571 B1

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

5

Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr
705 710 715 720

10

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 69

<211> 735

15

<212> PRT

<213> capsid protein of AAV serotype, clone A3.5

<400> 69

20

25

30

35

40

45

50

55

EP 1 310 571 B1

	Met	Ala	Ala	Asp	Gly	Tyr	Leu	Pro	Asp	Trp	Leu	Glu	Asp	Thr	Leu	Ser
	1				5					10					15	
5	Glu	Gly	Ile	Arg	Gln	Trp	Trp	Lys	Leu	Lys	Pro	Gly	Pro	Pro	Pro	Pro
				20					25				30			
	Lys	Pro	Asn	Gln	Gln	His	Arg	Asp	Asp	Ser	Arg	Gly	Leu	Val	Leu	Pro
10			35					40					45			
	Gly	Tyr	Lys	Tyr	Leu	Gly	Pro	Phe	Asn	Gly	Leu	Asp	Lys	Gly	Glu	Pro
		50					55					60				
15	Val	Asn	Glu	Ala	Asp	Ala	Ala	Ala	Leu	Glu	His	Asp	Lys	Ala	Tyr	Asp
	65					70					75					80
	His	Gln	Leu	Lys	Gln	Gly	Asp	Asn	Pro	Tyr	Leu	Lys	Tyr	Asn	His	Ala
20					85					90					95	
	Asp	Ala	Glu	Phe	Gln	Glu	Arg	Leu	Gln	Glu	Asp	Thr	Ser	Phe	Gly	Gly
				100					105					110		
25	Asn	Leu	Gly	Arg	Ala	Val	Phe	Gln	Ala	Lys	Lys	Arg	Val	Leu	Glu	Pro
			115					120					125			
	Leu	Gly	Leu	Val	Glu	Glu	Ala	Val	Lys	Thr	Ala	Pro	Gly	Lys	Lys	Arg
30		130					135					140				
	Pro	Ile	Glu	Gln	Ser	Pro	Ala	Glu	Pro	Asp	Ser	Ser	Ser	Gly	Ile	Gly
	145					150					155					160
35	Lys	Ser	Gly	Gln	Gln	Pro	Ala	Lys	Lys	Arg	Leu	Asn	Phe	Gly	Gln	Thr
				165						170					175	
	Gly	Asp	Thr	Glu	Ser	Val	Pro	Asp	Pro	Gln	Pro	Ile	Gly	Glu	Pro	Pro
40				180					185					190		

EP 1 310 571 B1

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
195 200 205

5 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

10 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

15 Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr
260 265 270

20 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
290 295 300

25 Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305 310 315 320

30 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
340 345 350

35 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365

40 Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400

45 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
405 410 415

50 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
435 440 445

55

EP 1 310 571 B1

Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Asn Gln.
 450 455 460
 5
 Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
 465 470 475 480
 10
 Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn
 485 490 495
 Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Pro Asn Gly
 500 505 510
 15
 Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Met Ala Ser His Lys Asp
 515 520 525
 20
 Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr
 545 550 555 560
 25
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Gln Val Ala Thr Asn Arg Gln Ser Gln Asn Thr Thr Ala Ser Tyr
 580 585 590
 30
 Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 35
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Thr Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 40
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 45
 Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 50
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 55

EP 1 310 571 B1

Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 70
<211> 735
<212> PRT
<213> capsid protein of AAV serotype, clone AAV2

<400> 70

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
25 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
30 65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
35 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
180 185 190

EP 1 310 571 B1

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
195 200 205

5 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

10 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

15 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
260 265 270

20 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
290 295 300

25 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305 310 315 320

30 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
340 345 350

35 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365

40 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400

45 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
405 410 415

50 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

55 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
435 440 445

EP 1 310 571 B1

5 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 10 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 15 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 20 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 25 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
 580 585 590
 30 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 35 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 40 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655
 45 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 50 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 55

EP 1 310 571 B1

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

5

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

10

<210> 71
<211> 736
<212> PRT
<213> capsid protein of AAV serotype, clone AAV3

15

<400> 71

20

25

30

35

40

45

50

55

EP 1 310 571 B1

	Met	Ala	Ala	Asp	Gly	Tyr	Leu	Pro	Asp	Trp	Leu	Glu	Asp	Asn	Leu	Ser
	1				5					10					15	
5	Glu	Gly	Ile	Arg	Glu	Trp	Trp	Ala	Leu	Lys	Pro	Gly	Val	Pro	Gln	Pro
				20					25					30		
	Lys	Ala	Asn	Gln	Gln	His	Gln	Asp	Asn	Arg	Arg	Gly	Leu	Val	Leu	Pro
10			35					40					45			
	Gly	Tyr	Lys	Tyr	Leu	Gly	Pro	Gly	Asn	Gly	Leu	Asp	Lys	Gly	Glu	Pro
		50					55					60				
15	Val	Asn	Glu	Ala	Asp	Ala	Ala	Ala	Leu	Glu	His	Asp	Lys	Ala	Tyr	Asp
	65					70					75					80
	Gln	Gln	Leu	Lys	Ala	Gly	Asp	Asn	Pro	Tyr	Leu	Lys	Tyr	Asn	His	Ala
20					85					90					95	
	Asp	Ala	Glu	Phe	Gln	Glu	Arg	Leu	Gln	Glu	Asp	Thr	Ser	Phe	Gly	Gly
				100					105					110		
25	Asn	Leu	Gly	Arg	Ala	Val	Phe	Gln	Ala	Lys	Lys	Arg	Ile	Leu	Glu	Pro
			115					120					125			
	Leu	Gly	Leu	Val	Glu	Glu	Ala	Ala	Lys	Thr	Ala	Pro	Gly	Lys	Lys	Gly
30		130					135					140				
	Ala	Val	Asp	Gln	Ser	Pro	Gln	Glu	Pro	Asp	Ser	Ser	Ser	Gly	Val	Gly
	145					150					155					160
35	Lys	Ser	Gly	Lys	Gln	Pro	Ala	Arg	Lys	Arg	Leu	Asn	Phe	Gly	Gln	Thr
					165					170					175	
	Gly	Asp	Ser	Glu	Ser	Val	Pro	Asp	Pro	Gln	Pro	Leu	Gly	Glu	Pro	Pro
40				180					185					190		
	Ala	Ala	Pro	Thr	Ser	Leu	Gly	Ser	Asn	Thr	Met	Ala	Ser	Gly	Gly	Gly
			195					200					205			

EP 1 310 571 B1

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

5 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

10 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
260 265 270

15 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

20 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
290 295 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305 310 315 320

25 Arg Gly Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

30 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365

35 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380

40 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
405 410 415

45 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

50 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
435 440 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
450 455 460

55

EP 1 310 571 B1

5 Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
485 490 495

10 Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
500 505 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
515 520 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
530 535 540

20 Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
565 570 575

25 Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
580 585 590

30 Thr Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

35 Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

40 Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

45 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

50 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

55 Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

EP 1 310 571 B1

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

5

<210> 72

<211> 737

<212> PRT

<213> capsid protein of AAV serotype, clone 3.3bVP1

10

<400> 72

15

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

20

Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
35 40 45

25

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

30

Gln Gln Leu Asn Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

35

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

40

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Ala Lys Lys Arg
130 135 140

45

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

50

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
180 185 190

55

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Val Ala Ala Gly Gly
195 200 205

EP 1 310 571 B1

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
 210 215 220
 5
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 10
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Glu Gln Ile Ser Ser Glu Thr Ala Gly Ser Thr Asn Asp Asn
 260 265 270
 15
 Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300
 20
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile
 305 310 315 320
 25
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
 325 330 335
 Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
 340 345 350
 30
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
 355 360 365
 35
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
 370 375 380
 Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400
 40
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser
 405 410 415
 45
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
 420 425 430
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
 435 440 445
 50
 Arg Thr Gln Ser Asp Pro Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
 450 455 460
 55

EP 1 310 571 B1

5
 Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
 465 470 475 480

10
 Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
 485 490 495

15
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510

20
 Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525

25
 His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
 530 535 540

30
 Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu
 545 550 555 560

35
 Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
 565 570 575

40
 Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
 580 585 590

45
 Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
 595 600 605

50
 Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
 610 615 620

55
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
 625 630 635 640

60
 Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
 645 650 655

65
 Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
 660 665 670

70
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
 675 680 685

75
 Gln Lys Glu Asn Ser Lys Arg Trp Asp Pro Glu Ile Gln Tyr Thr Ser
 690 695 700

80
 Asn Phe Glu Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
 705 710 715 720

EP 1 310 571 B1

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

5

Leu

<210> 73

10

<211> 644

<212> PRT

<213> capsid protein of AAV serotype, clone 223-4

<400> 73

15

Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1 5 10 15

20

Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr
20 25 30

Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
35 40 45

25

Val Leu Glu Pro Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro
50 55 60

30

Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65 70 75 80

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
85 90 95

35

Gly Asp Ser Glu Pro Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
100 105 110

40

Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
115 120 125

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
130 135 140

45

Ser Gly Asn Trp His Cys Asp Ser Thr Arg Leu Gly Asp Arg Val Ile
145 150 155 160

50

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
165 170 175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
180 185 190

55

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
195 200 205

EP 1 310 571 B1

5 His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
 210 215 220
 Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
 225 230 235 240
 10 Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
 245 250 255
 Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
 260 265 270
 15 Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
 275 280 285
 20 Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
 290 295 300
 Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
 305 310 315 320
 25 Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
 325 330 335
 30 Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly
 340 345 350
 Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
 355 360 365
 35 Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
 370 375 380
 40 Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp Leu
 385 390 395 400
 Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
 405 410 415
 45 Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
 420 425 430
 50 Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
 435 440 445
 55 Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
 450 455 460

EP 1 310 571 B1

5 Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465 470 475 480

Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
485 490

10 Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
500 505 510

Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
515 520 525

15 Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
530 535 540

20 Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545 550 555 560

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
565 570 575

25 Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr
580 585 590

30 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
595 600 605

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
610 615 620

35 Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625 630 635 640

40 Tyr Ser Glu Pro

<210> 74

<211> 644

<212> PRT

<213> capsid protein of AAV serotype, clone 223.5

<400> 74

EP 1 310 571 B1

Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
 1 5 10 15

5 Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr
 20 25 30

10 Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
 35 40 45

15

20

25

30

35

40

45

50

55

EP 1 310 571 B1

Val Leu Glu Pro Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro
50 55 60

5 Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65 70 75 80

10 Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
85 90 95

Gly Asp Ser Glu Pro Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
100 105 110

15 Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
115 120 125

20 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
130 135 140

Ser Gly Asn Trp His Cys Asp Ser Thr Arg Leu Gly Asp Arg Val Ile
145 150 155 160

25 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
165 170 175

30 Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
180 185 190

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
195 200 205

35 His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
210 215 220

40 Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225 230 235 240

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
245 250 255

45 Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
260 265 270

50 Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
275 280 285

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
290 295 300

EP 1 310 571 B1

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
 305 310 315 320
 5
 Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
 325 330 335
 10
 Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly
 340 345 350
 Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
 355 360 365
 15
 Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
 370 375 380
 Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp Leu
 385 390 395 400
 20
 Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
 405 410 415
 25
 Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
 420 425 430
 Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
 435 440 445
 30
 Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
 450 455 460
 35
 Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
 465 470 475 480
 Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
 485 490 495
 40
 Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
 500 505 510
 45
 Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
 515 520 525
 Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
 530 535 540
 50
 Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
 545 550 555 560
 55

EP 1 310 571 B1

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
 565 570 575
 5 Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr
 580 585 590
 10 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
 595 600 605
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
 610 615 620
 15 Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
 625 630 635 640
 Tyr Ser Glu Pro
 20
 <210> 75
 <211> 644
 <212> PRT
 25 <213> capsid protein of AAV serotype, clone 223.10
 <220>
 <221> MISC_FEATURE
 <222> (434)..(434)
 30 <223> can be any amino acid
 <400> 75
 35 Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
 1 5 10 15
 Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr
 20 25 30
 40 Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
 35 40 45
 45 Val Leu Glu Pro Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro
 50 55 60
 Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
 65 70 75 80
 50 Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
 85 90 95
 55 Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
 100 105 110

EP 1 310 571 B1

Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
115 120 125

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
130 135 140

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
145 150 155 160

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
165 170 175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
180 185 190

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
195 200 205

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
210 215 220

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225 230 235 240

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
245 250 255

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
260 265 270

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
275 280 285

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
290 295 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305 310 315 320

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
325 330 335

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
340 345 350

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
355 360 365

EP 1 310 571 B1

5 Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
370 375 380

10 Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp Leu
385 390 395 400

15 Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
405 410 415

20 Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
420 425 430

25 Asn Xaa Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
435 440 445

30 Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
450 455 460

35 Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465 470 475 480

40 Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
485 490 495

45 Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
500 505 510

50 Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
515 520 525

55 Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
530 535 540

60 Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545 550 555 560

65 Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
565 570 575

70 Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr
580 585 590

75 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
595 600 605

80 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
610 615 620

EP 1 310 571 B1

5 Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625 630 635 640

Tyr Ser Glu Pro

10 <210> 76
<211> 644
<212> PRT
<213> capsid protein of AAV serotype, clone 223.2

15 <400> 76

Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1 5 10 15

20 Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Cys Leu Gln Glu Asp Thr
20 25 30

Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
35 40 45

25 Val Leu Glu Pro Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro
50 55 60

30 Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65 70 75 80

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
85 90 95

35 Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
100 105 110

40 Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Val Ala Gly Gly Gly
115 120 125

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
130 135 140

45 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
145 150 155 160

50 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
165 170 175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
180 185 190

55 Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
195 200 205

EP 1 310 571 B1

5 His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
210 215 220

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225 230 235 240

10 Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
245 250 255

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
15 260 265 270

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
275 280 285

20 Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
290 295 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
25 305 310 315 320

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
325 330 335

30 Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
340 345 350

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
35 355 360 365

Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
370 375 380

40 Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp Leu
385 390 395 400

Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
45 405 410 415

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
420 425 430

50 Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
435 440 445

Lys Asp Asp Glu Glu Arg Phe Ser Pro Ser Ser Gly Val Leu Ile Phe
55 450 455 460

EP 1 310 571 B1

5 Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465 470 475 480

Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
485 490 495

10 Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
500 505 510

15 Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
515 520 525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
530 535 540

20 Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545 550 555 560

25 Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
565 570 575

Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr
580 585 590

30 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
595 600 605

35 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
610 615 620

Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625 630 635 640

40 Tyr Ser Glu Pro

<210> 77

<211> 644

<212> PRT

<213> capsid protein of AAV serotype, clone 223.7

<400> 77

50 Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1 5 10 15

Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr
20 25 30

EP 1 310 571 B1

Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
 35 40 45
 5
 Val Leu Glu Pro Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro
 50 55 60
 10
 Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
 65 70 75 80
 Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
 85 90 95
 15
 Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
 100 105 110
 20
 Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
 115 120 125
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
 130 135 140
 25
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
 145 150 155 160
 30
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 165 170 175
 Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
 180 185 190
 35
 Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
 195 200 205
 40
 His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
 210 215 220
 Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
 225 230 235 240
 45
 Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
 245 250 255
 50
 Leu Thr Ser Thr Val Gln Val Phe Ser Asp Pro Glu Tyr Gln Leu Pro
 260 265 270
 Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
 275 280 285
 55

EP 1 310 571 B1

5

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
290 295 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305 310 315 320

10

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
325 330 335

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
340 345 350

15

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
355 360 365

20

Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
370 375 380

Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp Leu
385 390 395 400

25

Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
405 410 415

30

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
420 425 430

Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
435 440 445

35

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
450 455 460

40

Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465 470 475 480

Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
485 490 495

45

Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
500 505 510

50

Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
515 520 525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
530 535 540

55

EP 1 310 571 B1

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545 550 555 560

5 Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
565 570 575

10 Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Ile Ala Ser Phe Ile Thr
580 585 590

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
595 600 605

15 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
610 615 620

20 Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625 630 635 640

Tyr Ser Glu Pro

25 <210> 78
<211> 644
<212> PRT
<213> capsid protein of AAV serotype, clone 223.6

30 <400> 78

Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1 5 10 15

35 Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr
20 25 30

40 Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
35 40 45

Val Leu Glu Pro Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro
50 55 60

45 Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65 70 75 80

50 Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
85 90 95

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
100 105 110

55 Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
115 120 125

EP 1 310 571 B1

Ala Pro Met Ala Asp Asn Ser Glu Gly Ala Asp Gly Val Gly Asn Ala
130 135 140

5 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
145 150 155 160

10 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
165 170 175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
180 185 190

15 Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
195 200 205

20 His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
210 215 220

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225 230 235 240

25 Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
245 250 255

30 Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
260 265 270

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
275 280 285

35 Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
290 295 300

40 Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305 310 315 320

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
325 330 335

45 Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
340 345 350

50 Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
355 360 365

Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
370 375 380

EP 1 310 571 B1

Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp Leu
 385 390 395 400

5 Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
 405 410 415

10 Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
 420 425 430

Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
 435 440 445

15 Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
 450 455 460

20 Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
 465 470 475 480

Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
 485 490 495

25 Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
 500 505 510

30 Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
 515 520 525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
 530 535 540

35 Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
 545 550 555 560

40 Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
 565 570 575

Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Leu Ala Ser Phe Ile Thr
 580 585 590

45 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
 595 600 605

50 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
 610 615 620

Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
 625 630 635 640

Tyr Ser Glu Pro

5

<210> 79

<211> 738

<212> PRT

10

<213> capsid protein of AAV serotype, clone 44.1

<400> 79

15

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

20

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

25

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

30

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

35

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

40

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

45

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

50

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

55

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

EP 1 310 571 B1

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 5
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 10
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 15
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 20
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
 305 310 315 320
 25
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 30
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 35
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 40
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
 405 410 415
 45
 Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 50
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
 450 455 460
 55

EP 1 310 571 B1

5

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
485 490 495

10

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
500 505 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
515 520 525

15

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
530 535 540

20

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545 550 555 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
565 570 575

25

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
580 585 590

30

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

35

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

40

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

45

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

50

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705 710 715 720

55

EP 1 310 571 B1

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

5

Asn Leu

10

<210> 80

<211> 738

<212> PRT

<213> capsid protein of AAV serotype, clone 44.5

15

<400> 80

20

25

30

35

40

45

50

55

EP 1 310 571 B1

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

5 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

10 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

15 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

20 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

25 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

30 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

35 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

40 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

45

50

55

EP 1 310 571 B1

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 5
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 10
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 15
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 20
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Pro Asn Phe Lys Leu Phe Asn
 305 310 315 320
 25
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 30
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 35
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 40
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
 405 410 415
 45
 Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 50
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
 450 455 460
 55

EP 1 310 571 B1

5

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
485 490 495

10

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
500 505 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
515 520 525

15

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
530 535 540

20

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545 550 555 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
565 570 575

25

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
580 585 590

30

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

35

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

40

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

45

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

50

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705 710 715 720

55

EP 1 310 571 B1

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

5

Asn Leu

10

<210> 81

<211> 738

<212> PRT

<213> capsid protein of AAV serotype, clone 44.2

15

<400> 81

20

25

30

35

40

45

50

55

EP 1 310 571 B1

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

5 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

10 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

15 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

20 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

25 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

30 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

35 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

40 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

45

50

55

EP 1 310 571 B1

5 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

10 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

15 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

20 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305 310 315 320

25 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

30 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

35 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

40 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
405 410 415

45 Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

50 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
450 455 460

EP 1 310 571 B1

5 Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 10 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 15 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
 530 535 540
 20 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 25 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
 580 585 590
 30 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 35 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 40 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
 660 665 670
 45 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 50 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
 705 710 715 720
 55

EP 1 310 571 B1

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

5

Asn Leu

10

<210> 82

<211> 738

<212> PRT

<213> capsid protein of AAV serotype, clone 29.3VP1

15

<400> 82

20

25

30

35

40

45

50

55

EP 1 310 571 B1

	Met	Ala	Ala	Asp	Gly	Tyr	Leu	Pro	Asp	Trp	Leu	Glu	Asp	Asn	Leu	Ser
	1				5					10					15	
5	Glu	Gly	Ile	Arg	Glu	Trp	Trp	Ala	Leu	Lys	Pro	Gly	Ala	Pro	Lys	Pro
				20					25					30		
	Lys	Ala	Asn	Gln	Gln	Lys	Gln	Asp	Asp	Gly	Arg	Gly	Leu	Val	Leu	Pro
10			35					40					45			
	Gly	Tyr	Lys	Tyr	Leu	Gly	Pro	Phe	Asn	Gly	Leu	Asp	Lys	Gly	Glu	Pro
		50					55					60				
15	Val	Asn	Ala	Ala	Asp	Ala	Ala	Ala	Leu	Glu	His	Asp	Lys	Ala	Tyr	Asp
	65					70					75					80
	Gln	Gln	Leu	Lys	Ala	Gly	Asp	Asn	Pro	Tyr	Leu	Arg	Tyr	Asn	His	Ala
20					85					90					95	
	Asp	Ala	Glu	Phe	Gln	Glu	Arg	Leu	Gln	Glu	Asp	Thr	Ser	Phe	Gly	Gly
				100					105					110		
25	Asn	Leu	Gly	Arg	Ala	Val	Phe	Gln	Ala	Lys	Lys	Arg	Val	Leu	Glu	Pro
			115					120					125			
	Leu	Gly	Leu	Val	Glu	Glu	Gly	Ala	Lys	Thr	Ala	Pro	Gly	Lys	Lys	Arg
30		130					135					140				
	Pro	Val	Glu	Pro	Ser	Pro	Gln	Arg	Ser	Pro	Asp	Ser	Thr	Thr	Gly	Ile
	145					150					155					160
35	Gly	Lys	Lys	Gly	Gln	Gln	Pro	Ala	Lys	Lys	Arg	Leu	Asn	Phe	Gly	Gln
					165					170					175	
	Thr	Gly	Asp	Ser	Glu	Ser	Val	Pro	Asp	Pro	Gln	Pro	Ile	Gly	Glu	Pro
40				180					185					190		
	Pro	Ala	Gly	Pro	Ser	Gly	Leu	Gly	Ser	Gly	Thr	Met	Ala	Ala	Gly	Gly
			195					200					205			
45																
50																
55																

EP 1 310 571 B1

5 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

10 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
15 260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

20 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
25 305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

30 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala Arg Gln Gly Cys Leu Pro Pro Phe
35 355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

40 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
45 405 410 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

50 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
55 450 455 460

EP 1 310 571 B1

5 Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
485 490 495

10 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
500 505 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
515 520 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
530 535 540

20 Phe Gly Lys Gln Gly Ala Gly Lys Gly Asn Val Asp Tyr Ser Ser Val
545 550 555 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
565 570 575

25 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
580 585 590

30 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

35 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

40 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

45 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

50 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

55 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705 710 715 720

EP 1 310 571 B1

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

5

Asn Leu

10

<210> 83

<211> 738

<212> PRT

<213> capsid protein of AAV serotype, clone 29.5VP1

15

<400> 83

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

20

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

25

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

30

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

35

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

40

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

45

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

50

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

55

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

EP 1 310 571 B1

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

5 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

10 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Gly Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

15 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

20 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

25 Asn Asn Trp Gly Phe Arg Pro Lys Ser Leu Asn Phe Lys Leu Phe Asn
305 310 315 320

30 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

35 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

40 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

45 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
405 410 415

50 Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

55

EP 1 310 571 B1

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
 450 455 460
 5
 Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
 465 470 475 480
 10
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asp Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 15
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
 530 535 540
 20
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
 545 550 555 560
 25
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
 580 585 590
 30
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 35
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 40
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
 660 665 670
 45
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 50
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 55

EP 1 310 571 B1

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705 710 715 720

5

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

10

Asn Leu

<210> 84

<211> 738

<212> PRT

15

<213> capsid protein of AAV serotype, clone 42.15

<400> 84

20

25

30

35

40

45

50

55

EP 1 310 571 B1

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

5
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

10
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

15
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

20
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

25
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

30
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

35
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

40
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

45
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

50
Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

55
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

EP 1 310 571 B1

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

5 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

10 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

15 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

20 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

25 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305 310 315 320

30 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

35 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Pro Pro Pro Phe
355 360 365

40 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

45 Phe Pro Ser Gln Met Arg Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
405 410 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

50 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

55

EP 1 310 571 B1

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
 450 455 460
 5
 Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
 465 470 475 480
 10
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 15
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
 530 535 540
 20
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
 545 550 555 560
 25
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
 580 585 590
 30
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 35
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 40
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 45
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
 660 665 670
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 50
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 55

EP 1 310 571 B1

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 85

<211> 738

<212> PRT

<213> capsid protein of AAV serotype, clone 42.8

<400> 85

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

EP 1 310 571 B1

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 5
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 10
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 15
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 20
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 25
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 30
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
 305 310 315 320
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 35
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 40
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 45
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 50
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
 405 410 415
 Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430

55

EP 1 310 571 B1

5 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
 450 455 460
 10 Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 15 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 20 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
 530 535 540
 25 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
 545 550 555 560
 30 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
 580 585 590
 35 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 40 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 45 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 50 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
 660 665 670
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685

EP 1 310 571 B1

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

5

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

10

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

15

<210> 86

<211> 733

<212> PRT

20

<213> amino acid of AAV serotype, clone 42.13

<400> 86

25

30

35

40

45

50

55

EP 1 310 571 B1

	Met	Ala	Ala	Asp	Gly	Tyr	Leu	Pro	Asp	Trp	Leu	Glu	Asp	Asn	Leu	Ser	
	1				5					10					15		
5	Glu	Gly	Ile	Arg	Glu	Trp	Trp	Asp	Leu	Lys	Pro	Gly	Ala	Pro	Lys	Pro	
				20					25					30			
	Lys	Ala	Asn	Gln	Gln	Lys	Gln	Asp	Asp	Gly	Arg	Gly	Leu	Val	Leu	Pro	
10			35					40					45				
	Gly	Tyr	Lys	Tyr	Leu	Gly	Pro	Phe	Asn	Gly	Leu	Asp	Lys	Gly	Glu	Pro	
		50					55					60					
15	Val	Asn	Ala	Ala	Asp	Ala	Ala	Ala	Leu	Glu	His	Asp	Lys	Ala	Tyr	Asp	
	65					70					75					80	
	Gln	Gln	Leu	Lys	Ala	Gly	Asp	Asn	Pro	Tyr	Leu	Arg	Tyr	Asn	His	Ala	
20					85					90					95		
	Asp	Ala	Glu	Phe	Gln	Glu	Arg	Leu	Gln	Glu	Asp	Thr	Ser	Phe	Gly	Gly	
				100					105					110			
25	Asn	Leu	Gly	Arg	Ala	Val	Phe	Gln	Ala	Lys	Lys	Arg	Val	Leu	Glu	Pro	
			115					120					125				
	Leu	Gly	Leu	Val	Glu	Glu	Gly	Ala	Lys	Thr	Ala	Pro	Gly	Lys	Lys	Arg	
30		130					135					140					
	Pro	Ile	Glu	Ser	Pro	Asp	Ser	Ser	Thr	Gly	Ile	Gly	Lys	Lys	Gly	Gln	
	145					150					155					160	
35	Gln	Pro	Ala	Lys	Lys	Lys	Leu	Asn	Phe	Gly	Gln	Thr	Gly	Asp	Ser	Glu	
					165					170					175		

EP 1 310 571 B1

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
 180 185 190
 Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
 195 200 205
 Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp
 210 215 220
 His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
 225 230 235 240
 Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
 245 250 255
 Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn Thr Tyr Phe Gly
 260 265 270
 Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His
 275 280 285
 Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe
 290 295 300
 Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu
 305 310 315 320
 Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser
 325 330 335
 Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu
 340 345 350
 Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe
 355 360 365
 Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala
 370 375 380
 Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met
 385 390 395 400
 Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe Glu Asp Val
 405 410 415
 Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met
 420 425 430

EP 1 310 571 B1

5

Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser
435 440 445

Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly
450 455 460

10

Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys
465 470 475 480

Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Ser Gln Asn Asn Asn Ser
485 490 495

15

Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp
500 505 510

20

Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His Lys Gly Asp Glu
515 520 525

Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly
530 535 540

25

Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val Met Leu Thr Ser Glu
545 550 555 560

30

Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val
565 570 575

Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro Ile Val Gly Ala
580 585 590

35

Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp
595 600 605

40

Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly
610 615 620

Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro
625 630 635 640

45

Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro
645 650 655

50

Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn
675 680 685

55

EP 1 310 571 B1

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys
690 695 700

Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu
705 710 715 720

Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Ser Leu
725 730

<210> 87

<211> 733

<212> PRT

<213> capsid protein of AAV serotype, clone 42.3A

<400> 87

EP 1 310 571 B1

	Met	Ala	Ala	Asp	Gly	His	Leu	Pro	Asp	Trp	Leu	Glu	Asp	Asn	Leu	Ser	
	1				5					10					15		
5	Glu	Gly	Ile	Arg	Glu	Trp	Trp	Asp	Leu	Lys	Pro	Gly	Ala	Pro	Lys	Pro	
				20					25					30			
	Lys	Ala	Asn	Gln	Gln	Lys	Gln	Asp	Asp	Gly	Arg	Gly	Leu	Val	Leu	Pro	
10			35					40					45				
	Gly	Tyr	Lys	Tyr	Leu	Gly	Pro	Phe	Asn	Gly	Leu	Asp	Lys	Gly	Glu	Pro	
		50					55					60					
15	Val	Asn	Ala	Ala	Asp	Ala	Ala	Ala	Leu	Glu	His	Asp	Lys	Ala	Tyr	Asp	
	65					70					75					80	
	Gln	Gln	Leu	Lys	Ala	Gly	Asp	Asn	Pro	Tyr	Leu	Arg	Tyr	Asn	His	Ala	
20				85						90					95		
	Asp	Ala	Glu	Phe	Gln	Glu	Arg	Leu	Gln	Glu	Asp	Thr	Ser	Phe	Gly	Gly	
				100					105					110			
25	Asn	Leu	Gly	Arg	Ala	Val	Phe	Gln	Ala	Lys	Lys	Arg	Val	Leu	Glu	Pro	
			115					120					125				
	Leu	Gly	Leu	Val	Glu	Glu	Gly	Ala	Lys	Thr	Ala	Pro	Gly	Lys	Lys	Arg	
30		130					135					140					
	Pro	Ile	Glu	Ser	Pro	Asp	Ser	Ser	Thr	Gly	Ile	Gly	Lys	Lys	Gly	Gln	
	145					150					155					160	
35	Gln	Pro	Ala	Lys	Lys	Lys	Leu	Asn	Phe	Gly	Gln	Thr	Gly	Asp	Ser	Glu	
				165						170					175		
	Ser	Val	Pro	Asp	Pro	Gln	Pro	Ile	Gly	Glu	Pro	Pro	Ala	Gly	Pro	Ser	
40				180					185					190			

EP 1 310 571 B1

5 Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
195 200 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp
210 215 220

10 His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225 230 235 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
245 250 255

15 Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn Thr Tyr Phe Gly
260 265 270

20 Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His
275 280 285

Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Ser Trp Gly Phe
290 295 300

25 Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu
305 310 315 320

30 Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser
325 330 335

Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu
340 345 350

35 Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe
355 360 365

40 Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala
370 375 380

Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met
385 390 395 400

45 Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe Glu Asp Val
405 410 415

50 Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met
420 425 430

Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser
435 440 445

55

EP 1 310 571 B1

5
 Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly
 450 455 460

10
 Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys
 465 470 475 480

15
 Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser Gln Asn Asn Asn Ser
 485 490 495

20
 Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp
 500 505 510

25
 Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu
 515 520 525

30
 Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly
 530 535 540

35
 Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val Met Leu Thr Ser Glu
 545 550 555 560

40
 Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val
 565 570 575

45
 Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro Ile Val Gly Ala
 580 585 590

50
 Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp
 595 600 605

55
 Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly
 610 615 620

60
 Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro
 625 630 635 640

65
 Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro
 645 650 655

70
 Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser
 660 665 670

75
 Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn
 675 680 685

80
 Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys
 690 695 700

EP 1 310 571 B1

Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu
705 710 715 720

5

Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

10

<210> 88
<211> 731
<212> PRT
<213> capsid protein of AAV serotype, clone 42.4

15

<400> 88

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

20

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

25

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

30

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

35

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

40

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

45

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145 150 155 160

50

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
165 170 175

55

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
180 185 190

EP 1 310 571 B1

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
 195 200 205
 5
 Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
 210 215 220
 10
 His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
 225 230 235 240
 Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
 245 250 255
 15
 Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
 260 265 270
 20
 Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
 275 280 285
 Ser Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
 290 295 300
 25
 Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
 305 310 315 320
 30
 Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
 325 330 335
 Gln Val Phe Thr Asp Ser Glu Tyr Arg Leu Pro Tyr Val Leu Gly Ser
 340 345 350
 35
 Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
 355 360 365
 40
 Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val Gly
 370 375 380
 Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
 385 390 395 400
 45
 Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe Glu Asp Val Pro Phe
 405 410 415
 50
 His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
 420 425 430
 Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser Thr Gly
 435 440 445
 55

EP 1 310 571 B1

5 Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly Pro Asn
450 455 460

Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg
465 470 475 480

10 Gln Gln Arg Val Ser Thr Thr Leu Ser Gln Asn Asn Asn Ser Asn Phe
485 490 495

Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu
500 505 510

Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg
515 520 525

20 Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly
530 535 540

Lys Asp Asn Val Asp Tyr Ser Ser Val Met Leu Thr Ser Glu Glu Glu
545 550 555 560

25 Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala
565 570 575

30 Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro Ile Val Gly Ala Val Asn
580 585 590

Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr
595 600 605

35 Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe
610 615 620

40 His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
625 630 635 640

Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Thr
645 650 655

45 Phe Ser Gln Ala Lys Pro Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
660 665 670

50 Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
675 680 685

Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Thr
690 695 700

55

EP 1 310 571 B1

Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu Pro Arg
705 710 715 720

5

Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

10

<210> 89

<211> 731

<212> PRT

<213> capsid protein of AAV serotype, clone 42.5A

15

<400> 89

20

25

30

35

40

45

50

55

EP 1 310 571 B1

	Met	Ala	Ala	Asp	Gly	Tyr	Leu	Pro	Asp	Trp	Leu	Glu	Asp	Asn	Leu	Ser	
	1				5					10					15		
5	Glu	Gly	Ile	Arg	Glu	Trp	Trp	Asp	Leu	Lys	Pro	Gly	Ala	Pro	Lys	Pro	
				20					25					30			
	Lys	Ala	Asn	Gln	Gln	Lys	Gln	Asp	Asp	Gly	Arg	Gly	Leu	Val	Leu	Pro	
			35					40					45				
10	Gly	Tyr	Lys	Tyr	Leu	Gly	Pro	Phe	Asn	Gly	Leu	Asp	Lys	Gly	Glu	Pro	
		50					55					60					
	Val	Asn	Glu	Ala	Asp	Ala	Ala	Ala	Leu	Glu	His	Asp	Lys	Ala	Tyr	Asp	
15		65				70					75					80	
	Lys	Gln	Leu	Glu	Gln	Gly	Asp	Asn	Pro	Tyr	Leu	Lys	Tyr	Asn	His	Ala	
					85					90					95		
20	Asp	Ala	Glu	Phe	Gln	Glu	Arg	Leu	Gln	Glu	Asp	Thr	Ser	Phe	Gly	Gly	
				100					105					110			
	Asn	Leu	Gly	Arg	Ala	Val	Phe	Arg	Ala	Lys	Lys	Arg	Val	Leu	Glu	Pro	
25			115					120					125				
	Leu	Gly	Leu	Val	Glu	Glu	Gly	Ala	Lys	Thr	Ala	Pro	Gly	Lys	Lys	Arg	
		130					135					140					
30	Pro	Ile	Glu	Ser	Pro	Asp	Ser	Ser	Thr	Gly	Ile	Gly	Lys	Lys	Gly	Gln	
		145				150					155					160	
	Gln	Pro	Ala	Lys	Lys	Lys	Leu	Asn	Phe	Gly	Gln	Thr	Gly	Asp	Ser	Glu	
35					165					170					175		
	Ser	Val	Pro	Asp	Pro	Gln	Pro	Leu	Gly	Glu	Pro	Pro	Ala	Ala	Pro	Ser	
				180					185					190			
40	Gly	Leu	Gly	Ser	Gly	Thr	Met	Ala	Ala	Gly	Gly	Gly	Ala	Pro	Met	Ala	
			195					200					205				

EP 1 310 571 B1

5

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
210 215 220

10

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225 230 235 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
245 250 255

15

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
260 265 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
275 280 285

20

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Arg Gly Phe Arg Pro
290 295 300

25

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305 310 315 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
325 330 335

30

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
340 345 350

35

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
355 360 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
370 375 380

40

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385 390 395 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe Glu Asp Val Pro Phe
405 410 415

45

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
420 425 430

50

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser Thr Gly
435 440 445

Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly Pro Asn
450 455 460

55

EP 1 310 571 B1

	Asn	Met	Ser	Ala	Gln	Ala	Lys	Asn	Trp	Leu	Pro	Gly	Pro	Cys	Tyr	Arg
	465					470					475					480
5	Gln	Gln	Arg	Val	Ser	Thr	Thr	Leu	Ser	Gln	Asn	Asn	Asn	Ser	Asn	Phe
					485					490					495	
10	Ala	Trp	Thr	Gly	Ala	Thr	Lys	Tyr	His	Leu	Asn	Gly	Arg	Asp	Ser	Leu
				500					505					510		
15	Val	Asn	Pro	Gly	Val	Ala	Met	Ala	Thr	His	Lys	Asp	Asp	Glu	Glu	Arg
			515					520					525			
20	Phe	Phe	Pro	Ser	Ser	Gly	Val	Leu	Met	Phe	Gly	Lys	Gln	Gly	Ala	Gly
	530						535					540				
25	Lys	Asp	Asn	Val	Asp	Tyr	Ser	Ser	Val	Met	Leu	Thr	Ser	Glu	Glu	Glu
	545					550					555					560
30	Ile	Lys	Thr	Thr	Asn	Pro	Val	Ala	Thr	Glu	Gln	Tyr	Gly	Val	Val	Ala
					565					570					575	
35	Asp	Asn	Leu	Gln	Gln	Gln	Asn	Ala	Ala	Pro	Ile	Val	Gly	Ala	Val	Asn
				580					585					590		
40	Ser	Gln	Gly	Ala	Leu	Pro	Gly	Met	Ala	Trp	Gln	Asn	Arg	Asp	Val	Tyr
			595					600					605			
45	Leu	Gln	Gly	Pro	Ile	Trp	Ala	Lys	Ile	Pro	His	Thr	Asp	Gly	Asn	Phe
	610						615					620				
50	His	Pro	Ser	Pro	Leu	Met	Gly	Gly	Phe	Gly	Leu	Lys	His	Pro	Pro	Pro
	625					630					635					640
55	Gln	Ile	Leu	Ile	Lys	Asn	Thr	Pro	Val	Pro	Ala	Asp	Pro	Pro	Thr	Thr
					645					650					655	
60	Phe	Ser	Gln	Ala	Lys	Leu	Ala	Ser	Phe	Ile	Thr	Gln	Tyr	Ser	Thr	Gly
				660					665					670		
65	Gln	Val	Ser	Val	Glu	Ile	Glu	Trp	Glu	Leu	Gln	Lys	Glu	Asn	Ser	Lys
			675					680					685			
70	Arg	Trp	Asn	Pro	Glu	Ile	Gln	Tyr	Thr	Ser	Asn	Tyr	Tyr	Lys	Ser	Thr
	690						695					700				
75	Asn	Val	Asp	Phe	Ala	Val	Asn	Thr	Glu	Gly	Thr	Tyr	Ser	Glu	Pro	Arg
	705					710					715					720

EP 1 310 571 B1

Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

5

<210> 90

<211> 733

<212> PRT

<213> capsid protein of AAV serotype, clone 42.1B

10

<400> 90

15

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Arg Pro Gly Ala Pro Lys Pro
20 25 30

20

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

25

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

30

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

35

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

40

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145 150 155 160

45

Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
165 170 175

50

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
180 185 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
195 200 205

55

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp
210 215 220

EP 1 310 571 B1

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
 225 230 235 240
 5
 Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
 245 250 255
 10
 Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn Thr Tyr Phe Gly
 260 265 270
 Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His
 275 280 285
 15
 Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe
 290 295 300
 20
 Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu
 305 310 315 320
 Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser
 325 330 335
 25
 Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu
 340 345 350
 Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe
 355 360 365
 30
 Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala
 370 375 380
 35
 Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met
 385 390 395 400
 Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe Glu Asp Val
 405 410 415
 40
 Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met
 420 425 430
 45
 Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser
 435 440 445
 Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly
 450 455 460
 50
 Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys
 465 470 475 480
 55

EP 1 310 571 B1

5 Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Ser Gln Asn Asn Asn Ser
485 490 495

Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp
500 505 510

10 Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His Lys Gly Asp Glu
515 520 525

Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly
530 535 540

15 Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val Met Leu Thr Ser Glu
545 550 555 560

20 Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val
565 570 575

Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro Ile Val Gly Ala
580 585 590

25 Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp
595 600 605

30 Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly
610 615 620

Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro
625 630 635 640

35 Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro
645 650 655

40 Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn
675 680 685

45 Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys
690 695 700

50 Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu
705 710 715 720

Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

<210> 91

EP 1 310 571 B1

<211> 738

<212> PRT

<213> capsid protein of AAV serotype, clone 42.5B

5 <400> 91

```

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1          5          10          15

10 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
    20          25          30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
    35          40          45

15 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50          55          60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65          70          75          80

20 Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
    85          90          95

25 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
    100          105          110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
    115          120          125

30 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130          135          140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
35 145          150          155          160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
    165          170          175

40 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
    180          185          190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
45 195          200          205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210          215          220

50 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
    225          230          235          240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
55 245          250          255

```

EP 1 310 571 B1

5 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 10 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
 305 310 315 320
 15 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 20 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 25 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 30 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
 405 410 415
 35 Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 40 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
 450 455 460
 45 Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 50 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510

55

EP 1 310 571 B1

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
515 520 525

5 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
530 535 540

10 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545 550 555 560

Met Leu Thr Ser Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
565 570 575

15 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
580 585 590

20 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

25 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

30 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

35 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

40 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

45 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

50 <210> 92
<211> 738

<212> PRT

<213> capsid protein of AAV serotype, clone 43.1

55 <400> 92

EP 1 310 571 B1

	Met	Ala	Ala	Asp	Gly	Tyr	Leu	Pro	Asp	Trp	Leu	Glu	Asp	Asn	Leu	Ser	
	1				5					10					15		
5	Glu	Gly	Ile	Arg	Glu	Trp	Trp	Asp	Leu	Lys	Pro	Gly	Ala	Pro	Lys	Pro	
				20					25					30			
	Lys	Ala	Asn	Gln	Gln	Lys	Gln	Asp	Asp	Gly	Arg	Gly	Leu	Val	Leu	Pro	
10			35					40					45				
	Gly	Tyr	Lys	Tyr	Leu	Gly	Pro	Phe	Asn	Gly	Leu	Asp	Lys	Gly	Glu	Pro	
		50					55					60					
15	Val	Asn	Ala	Ala	Asp	Ala	Ala	Ala	Leu	Glu	His	Asp	Lys	Ala	Tyr	Asp	
	65					70					75					80	
	Gln	Gln	Leu	Lys	Ala	Gly	Asp	Asn	Pro	Tyr	Leu	Arg	Tyr	Asn	His	Ala	
20					85					90					95		
	Asp	Ala	Glu	Phe	Gln	Glu	Arg	Leu	Gln	Glu	Asp	Thr	Ser	Phe	Gly	Gly	
				100					105						110		
25	Asn	Leu	Gly	Arg	Ala	Val	Phe	Gln	Ala	Lys	Lys	Arg	Val	Leu	Glu	Pro	
			115					120					125				
	Leu	Gly	Leu	Val	Glu	Glu	Gly	Ala	Lys	Thr	Ala	Pro	Gly	Lys	Lys	Arg	
30		130					135					140					
	Pro	Val	Glu	Pro	Ser	Pro	Gln	Arg	Ser	Pro	Asp	Ser	Ser	Thr	Gly	Ile	
	145					150					155					160	
35	Gly	Lys	Lys	Gly	His	Gln	Pro	Ala	Arg	Lys	Arg	Leu	Asn	Phe	Gly	Gln	
					165					170					175		
	Thr	Gly	Asp	Ser	Glu	Ser	Val	Pro	Asp	Pro	Gln	Pro	Ile	Gly	Glu	Pro	
40				180					185					190			
	Pro	Ala	Gly	Pro	Ser	Gly	Leu	Gly	Ser	Gly	Thr	Met	Ala	Ala	Gly	Gly	
			195				200						205				
45	Gly	Ala	Pro	Met	Ala	Asp	Asn	Asn	Glu	Gly	Ala	Asp	Gly	Val	Gly	Ser	
		210					215					220					
	Ser	Ser	Gly	Asn	Trp	His	Cys	Asp	Ser	Thr	Trp	Leu	Gly	Asp	Arg	Val	
50	225					230					235					240	
	Ile	Thr	Thr	Ser	Thr	Arg	Thr	Trp	Ala	Leu	Pro	Thr	Tyr	Asn	Asn	His	
					245					250					255		

EP 1 310 571 B1

5 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 10 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
 305 310 315 320
 15 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 20 Leu Pro Tyr Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 25 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 30 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
 405 410 415
 35 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 40 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
 450 455 460
 45 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 50 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 55 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525

EP 1 310 571 B1

5 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
 530 535 540
 10 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
 545 550 555 560
 15 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 20 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala
 580 585 590
 25 Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 30 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 35 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 40 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Val Lys Asn Thr Pro Val
 645 650 655
 45 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
 660 665 670
 50 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 55 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 60 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720
 65 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735
 70 Asn Leu

<210> 93

<211> 738

<212> PRT

<213> capsid protein of AAV serotype, clone 43.12

<400> 93

EP 1 310 571 B1

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

5 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

10 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

15 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

20 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

25 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

30 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

35 Gly Lys Lys Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

40 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

45 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

50 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

55

EP 1 310 571 B1

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 5
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 10
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
 305 310 315 320
 15
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 20
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 25
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 30
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
 405 410 415
 35
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 40
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
 450 455 460
 45
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
 465 470 475 480
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495
 50
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510
 55

EP 1 310 571 B1

5 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
 530 535 540
 10 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 15 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala
 580 585 590
 Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 20 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 25 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Val Lys Asn Thr Pro Val
 645 650 655
 30 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
 660 665 670
 35 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 40 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720
 45 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735

Asn Leu

<210> 94

<211> 738

<212> PRT

<213> capsid protein of AAV serotype, clone 43.5

<400> 94

EP 1 310 571 B1

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

5 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

10 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

15 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

20 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

25 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

30 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

35 Gly Lys Lys Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

40 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

45 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

50 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

55

EP 1 310 571 B1

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

5 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

10 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305 310 315 320

15 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

20 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

25 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

30 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
405 410 415

35 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

40 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
450 455 460

45 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465 470 475 480

50 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
500 505 510

EP 1 310 571 B1

5 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
 530 535 540
 10 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
 545 550 555 560
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 15 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala
 580 585 590
 20 Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 25 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 30 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Val Lys Asn Thr Pro Val
 645 650 655
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
 660 665 670
 35 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 40 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720
 45 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735
 50 Asn Leu

<210> 95

<211> 738

<212> PRT

<213> capsid protein of AAV serotype, clone AAV8

<400> 95

EP 1 310 571 B1

	Met	Ala	Ala	Asp	Gly	Tyr	Leu	Pro	Asp	Trp	Leu	Glu	Asp	Asn	Leu	Ser
	1				5					10					15	
5	Glu	Gly	Ile	Arg	Glu	Trp	Trp	Ala	Leu	Lys	Pro	Gly	Ala	Pro	Lys	Pro
				20					25					30		
	Lys	Ala	Asn	Gln	Gln	Lys	Gln	Asp	Asp	Gly	Arg	Gly	Leu	Val	Leu	Pro
10			35					40					45			
	Gly	Tyr	Lys	Tyr	Leu	Gly	Pro	Phe	Asn	Gly	Leu	Asp	Lys	Gly	Glu	Pro
	50						55					60				
15	Val	Asn	Ala	Ala	Asp	Ala	Ala	Ala	Leu	Glu	His	Asp	Lys	Ala	Tyr	Asp
	65					70					75					80
	Gln	Gln	Leu	Gln	Ala	Gly	Asp	Asn	Pro	Tyr	Leu	Arg	Tyr	Asn	His	Ala
20					85					90					95	
	Asp	Ala	Glu	Phe	Gln	Glu	Arg	Leu	Gln	Glu	Asp	Thr	Ser	Phe	Gly	Gly
				100					105					110		
25	Asn	Leu	Gly	Arg	Ala	Val	Phe	Gln	Ala	Lys	Lys	Arg	Val	Leu	Glu	Pro
			115					120					125			
	Leu	Gly	Leu	Val	Glu	Glu	Gly	Ala	Lys	Thr	Ala	Pro	Gly	Lys	Lys	Arg
30		130					135					140				
	Pro	Val	Glu	Pro	Ser	Pro	Gln	Arg	Ser	Pro	Asp	Ser	Ser	Thr	Gly	Ile
	145					150					155					160
35	Gly	Lys	Lys	Gly	Gln	Gln	Pro	Ala	Arg	Lys	Arg	Leu	Asn	Phe	Gly	Gln
					165					170					175	
	Thr	Gly	Asp	Ser	Glu	Ser	Val	Pro	Asp	Pro	Gln	Pro	Leu	Gly	Glu	Pro
40				180					185					190		
	Pro	Ala	Ala	Pro	Ser	Gly	Val	Gly	Pro	Asn	Thr	Met	Ala	Ala	Gly	Gly
				195				200					205			
45	Gly	Ala	Pro	Met	Ala	Asp	Asn	Asn	Glu	Gly	Ala	Asp	Gly	Val	Gly	Ser
	210						215					220				
	Ser	Ser	Gly	Asn	Trp	His	Cys	Asp	Ser	Thr	Trp	Leu	Gly	Asp	Arg	Val
50	225				230						235					240

EP 1 310 571 B1

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 5
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp
 260 265 270
 10
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 15
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
 305 310 315 320
 20
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 25
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365
 30
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
 370 375 380
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400
 35
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
 405 410 415
 40
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445
 45
 Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
 450 455 460
 50
 Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
 465 470 475 480
 55
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
 485 490 495

EP 1 310 571 B1

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
 500 505 510
 5
 Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
 515 520 525
 10
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
 530 535 540
 Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
 545 550 555 560
 15
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575
 20
 Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
 580 585 590
 Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605
 25
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620
 30
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655
 35
 Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
 660 665 670
 40
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
 675 680 685
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
 690 695 700
 45
 Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
 705 710 715 720
 50
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
 725 730 735
 Asn Leu

55

<210> 96
 <211> 736

EP 1 310 571 B1

<212> PRT

<213> capsid protein of AAV serotype, clone 43.21

<400> 96

5

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

10

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

15

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

20

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

25

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

30

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

35

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

40

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

45

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
195 200 205

50

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

55

EP 1 310 571 B1

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 5
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 10
 Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
 260 265 270
 Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285
 15
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300
 20
 Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
 305 310 315 320
 Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
 325 330 335
 25
 Asn Leu Thr Ser Thr Val Arg Val Phe Thr Asp Ser Glu Tyr Gln Leu
 340 345 350
 30
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
 355 360 365
 Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
 370 375 380
 35
 Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400
 40
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
 405 410 415
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
 420 425 430
 45
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
 435 440 445
 50
 Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
 450 455 460
 55
 Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
 465 470 475 480

EP 1 310 571 B1

	Gly	Pro	Cys	Tyr	Arg	Gln	Gln	Arg	Val	Ser	Thr	Thr	Thr	Asn	Gln	Ser	
					485					490					495		
5	Asn	Asn	Ser	Asn	Phe	Ala	Trp	Thr	Gly	Ala	Ala	Lys	Phe	Lys	Leu	Asn	
				500					505					510			
	Gly	Arg	Asp	Ser	Leu	Met	Asn	Pro	Gly	Val	Ala	Met	Ala	Ser	His	Lys	
10			515					520					525				
	Asp	Asp	Asp	Asp	Arg	Phe	Phe	Pro	Ser	Ser	Gly	Val	Leu	Ile	Phe	Gly	
		530					535					540					
15	Lys	Gln	Gly	Ala	Gly	Asn	Asp	Gly	Val	Asp	Tyr	Ser	Gln	Val	Leu	Ile	
	545					550					555					560	
	Thr	Asp	Glu	Glu	Glu	Ile	Lys	Ala	Thr	Asn	Pro	Val	Ala	Thr	Glu	Glu	
20					565					570					575		
	Tyr	Gly	Ala	Val	Ala	Ile	Asn	Asn	Gln	Ala	Ala	Asn	Thr	Gln	Ala	Gln	
				580					585					590			
25	Thr	Gly	Leu	Val	His	Asn	Gln	Gly	Val	Ile	Pro	Gly	Met	Val	Trp	Gln	
			595					600					605				
	Asn	Arg	Asp	Val	Tyr	Leu	Gln	Gly	Pro	Ile	Trp	Ala	Lys	Ile	Pro	His	
30		610					615					620					
	Thr	Asp	Gly	Asn	Phe	His	Pro	Ser	Pro	Leu	Met	Gly	Gly	Phe	Gly	Leu	
	625					630					635					640	
35	Lys	His	Pro	Pro	Pro	Gln	Ile	Leu	Ile	Lys	Asn	Thr	Pro	Val	Pro	Ala	
					645					650					655		
	Asp	Pro	Pro	Leu	Thr	Phe	Asn	Gln	Ala	Lys	Leu	Asn	Ser	Phe	Ile	Thr	
40				660					665					670			
	Gln	Tyr	Ser	Thr	Gly	Gln	Val	Ser	Val	Glu	Ile	Glu	Trp	Glu	Leu	Gln	
			675					680					685				
45	Lys	Glu	Asn	Ser	Lys	Arg	Trp	Asn	Pro	Glu	Ile	Gln	Tyr	Thr	Ser	Asn	
	690						695					700					
	Tyr	Tyr	Lys	Ser	Thr	Asn	Val	Asp	Phe	Ala	Val	Asn	Thr	Glu	Gly	Val	
50	705					710					715					720	
	Tyr	Ser	Glu	Pro	Arg	Pro	Ile	Gly	Thr	Arg	Tyr	Leu	Thr	Arg	Asn	Leu	
					725					730					735		

<210> 97
<211> 736

EP 1 310 571 B1

<212> PRT

<213> capsid protein of AAV serotype, clone 43.25

<400> 97

5

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

10

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

15

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

20

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

25

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

30

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

35

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

40

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

45

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
195 200 205

50

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225 230 235 240

55

EP 1 310 571 B1

5 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

10 Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
260 265 270

15 Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

20 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

25 Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

30 Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
325 330 335

35 Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
340 345 350

40 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
355 360 365

45 Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
370 375 380

50 Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

55 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
405 410 415

60 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

65 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
435 440 445

70 Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
450 455 460

75 Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465 470 475 480

80 Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
485 490 495

EP 1 310 571 B1

5 Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
 500 505 510
 Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
 515 520 525
 10 Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
 530 535 540
 Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
 545 550 555 560
 15 Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
 565 570 575
 20 Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
 580 585 590
 Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
 595 600 605
 25 Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
 610 615 620
 30 Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
 625 630 635 640
 Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
 645 650 655
 35 Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
 660 665 670
 40 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
 675 680 685
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
 690 695 700
 45 Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
 705 710 715 720
 50 Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 98

<211> 736

<212> PRT

<213> capsid protein of AAV serotype, clone 43.23

EP 1 310 571 B1

<400> 98

5 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 10 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 15 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 20 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 25 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 30 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
 145 150 155 160
 35 Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 40 Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
 195 200 205
 45 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 50 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 55

EP 1 310 571 B1

5 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
260 265 270

10 Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

15 Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

20 Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
325 330 335

25 Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Leu Glu Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
355 360 365

30 Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
370 375 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

35 Pro Ser Gln Met Pro Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
405 410 415

40 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

45 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
435 440 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
450 455 460

50 Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
485 490 495

55

EP 1 310 571 B1

5 Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
 500 505 510

 10 Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
 515 520 525

 15 Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
 530 535 540

 20 Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
 545 550 555 560

 25 Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
 565 570 575

 30 Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
 580 585 590

 35 Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
 595 600 605

 40 Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
 610 615 620

 45 Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
 625 630 635 640

 50 Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
 645 650 655

 55 Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
 660 665 670

 60 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
 675 680 685

 65 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
 690 695 700

 70 Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
 705 710 715 720

 75 Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 99

<211> 736

<212> PRT

<213> capsid protein of AAV serotype, clone 43.20

EP 1 310 571 B1

<400> 99

5 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 10 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 15 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 20 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 25 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 30 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Leu Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
 145 150 155 160
 35 Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 40 Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
 195 200 205
 45 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 50 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 55

EP 1 310 571 B1

5 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

10 Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
260 265 270

15 Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

20 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

25 Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

30 Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
325 330 335

35 Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
340 345 350

40 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
355 360 365

45 Ala Asp Val Phe Thr Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
370 375 380

50 Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

55 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
405 410 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
435 440 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
450 455 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
485 490 495

EP 1 310 571 B1

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
 500 505 510
 5
 Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
 515 520 525
 10
 Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
 530 535 540
 15
 Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
 545 550 555 560
 20
 Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
 565 570 575
 Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
 580 585 590
 25
 Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
 595 600 605
 Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
 610 615 620
 30
 Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
 625 630 635 640
 Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
 645 650 655
 35
 Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
 660 665 670
 40
 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
 675 680 685
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
 690 695 700
 45
 Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
 705 710 715 720
 50
 Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 100

<211> 736

<212> PRT

<213> capsid protein of AAV serotype, clone AAV9

400> 100

EP 1 310 571 B1

	Met	Ala	Ala	Asp	Gly	Tyr	Leu	Pro	Asp	Trp	Leu	Glu	Asp	Asn	Leu	Ser	
	1				5					10					15		
5	Glu	Gly	Ile	Arg	Glu	Trp	Trp	Asp	Leu	Lys	Pro	Gly	Ala	Pro	Lys	Pro	
				20					25					30			
	Lys	Ala	Asn	Gln	Gln	Lys	Gln	Asp	Asp	Gly	Arg	Gly	Leu	Val	Leu	Pro	
10			35					40					45				
	Gly	Tyr	Lys	Tyr	Leu	Gly	Pro	Phe	Asn	Gly	Leu	Asp	Lys	Gly	Glu	Pro	
		50					55					60					
15	Val	Asn	Ala	Ala	Asp	Ala	Ala	Ala	Leu	Glu	His	Asp	Lys	Ala	Tyr	Asp	
	65					70					75					80	
	Gln	Gln	Leu	Lys	Ala	Gly	Asp	Asn	Pro	Tyr	Leu	Arg	Tyr	Asn	His	Ala	
20					85				90						95		
	Asp	Ala	Glu	Phe	Gln	Glu	Arg	Leu	Gln	Glu	Asp	Thr	Ser	Phe	Gly	Gly	
				100					105					110			
25	Asn	Leu	Gly	Arg	Ala	Val	Phe	Gln	Ala	Lys	Lys	Arg	Val	Leu	Glu	Pro	
			115					120					125				
	Leu	Gly	Leu	Val	Glu	Glu	Gly	Ala	Lys	Thr	Ala	Pro	Gly	Lys	Lys	Arg	
30		130					135					140					
	Pro	Val	Glu	Gln	Ser	Pro	Gln	Glu	Pro	Asp	Ser	Ser	Ser	Gly	Ile	Gly	
	145					150					155					160	
35	Lys	Ser	Gly	Gln	Gln	Pro	Ala	Lys	Lys	Arg	Leu	Asn	Phe	Gly	Gln	Thr	
				165						170					175		
	Gly	Asp	Ser	Glu	Ser	Val	Pro	Asp	Pro	Gln	Pro	Leu	Gly	Glu	Pro	Pro	
40				180					185					190			
	Glu	Ala	Pro	Ser	Gly	Leu	Gly	Pro	Asn	Thr	Met	Ala	Ser	Gly	Gly	Gly	
			195					200					205				
45	Ala	Pro	Met	Ala	Asp	Asn	Asn	Glu	Gly	Ala	Asp	Gly	Val	Gly	Asn	Ser	
		210					215					220					
	Ser	Gly	Asn	Trp	His	Cys	Asp	Ser	Thr	Trp	Leu	Gly	Asp	Arg	Val	Ile	
50		225				230					235					240	
	Thr	Thr	Ser	Thr	Arg	Thr	Trp	Ala	Leu	Pro	Thr	Tyr	Asn	Asn	His	Leu	
				245						250					255		

EP 1 310 571 B1

5 Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
260 265 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

10 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

15 Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
325 330 335

20 Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
340 345 350

25 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
370 375 380

30 Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

35 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
405 410 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

40 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
435 440 445

45 Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
450 455 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465 470 475 480

50 Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
485 490 495

55 Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
500 505 510

EP 1 310 571 B1

5 Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
515 520 525

Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
530 535 540

10 Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
565 570 575

15 Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
580 585 590

20 Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
595 600 605

25 Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

30 Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

35 Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

40 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

45 Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 101

<211> 728

<212> PRT

<213> capsid protein of AAV serotype, clone 24.1

<400> 101

EP 1 310 571 B1

Met	Ala	Ala	Asp	Gly	Tyr	Leu	Pro	Asp	Trp	Leu	Glu	Asp	Asn	Leu	Ser
1				5					10					15	

5

10

15

20

25

30

35

40

45

50

55

EP 1 310 571 B1

5
 10
 15
 20
 25
 30
 35
 40
 45
 50
 55

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45

Gly Tyr Lys Tyr Leu Arg Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125

Leu Gly Leu Val Glu Glu Val Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
 145 150 155 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
 165 170 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
 180 185 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
 195 200 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
 210 215 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
 225 230 235 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
 245 250 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Ser Tyr Ser
 260 265 270

EP 1 310 571 B1

5

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
275 280 285

10

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
290 295 300

15

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305 310 315 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
325 330 335

20

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
340 345 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
355 360 365

25

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
370 375 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385 390 395 400

30

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
405 410 415

His Ser Ser Tyr Val His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
420 425 430

35

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
435 440 445

40

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
450 455 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465 470 475 480

45

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
485 490 495

50

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
500 505 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
515 520 525

55

EP 1 310 571 B1

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
 530 535 540
 5
 Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
 545 550 555 560
 10
 Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
 565 570 575
 Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
 580 585 590
 15
 Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Cys Leu Gln Gly
 595 600 605
 20
 Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
 610 615 620
 Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
 625 630 635 640
 25
 Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
 645 650 655
 30
 Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
 660 665 670
 Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
 675 680 685
 35
 Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
 690 695 700
 40
 Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
 705 710 715 720
 Thr Arg Tyr Leu Thr Arg Asn Leu
 725
 45
 <210> 102
 <211> 728
 <212> PRT
 <213> capsid protein of AAV serotype, clone 42.2REAL
 50
 <400> 102
 55
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15

EP 1 310 571 B1

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 5
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 10
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 15
 Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 20
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 25
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 30
 Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
 145 150 155 160
 Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
 165 170 175
 35
 Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
 180 185 190
 40
 Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
 195 200 205
 Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
 210 215 220
 45
 His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
 225 230 235 240
 50
 Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
 245 250 255
 Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
 260 265 270
 55

EP 1 310 571 B1

5
 Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
 275 280 285

10
 Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
 290 295 300

15
 Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
 325 330 335

20
 Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
 340 345 350

25
 Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
 355 360 365

30
 Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
 370 375 380

35
 Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
 385 390 395 400

40
 Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
 405 410 415

45
 His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
 420 425 430

50
 Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
 435 440 445

55
 Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
 450 455 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
 465 470 475 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
 485 490 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
 500 505 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
 515 520 525

EP 1 310 571 B1

5 Pro Ile Asn Gly Val Leu Val Phe Gly Glu Thr Gly Ala Ala Asn Lys
 530 535 540
 Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
 545 550 555
 10 Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
 565 570 575
 Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
 580 585 590
 15 Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
 595 600 605
 20 Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
 610 615 620
 Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
 625 630 635
 25 Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
 645 650 655
 30 Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
 660 665 670
 Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
 675 680 685
 35 Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
 690 695 700
 40 Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
 705 710 715 720
 Thr Arg Tyr Leu Thr Arg Asn Leu
 725

45
 <210> 103
 <211> 728
 <212> PRT
 50 <213> capsid protein of AAV serotype, clone 7.2VP1
 <400> 103

55

EP 1 310 571 B1

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Gly Asn Leu Ser
1 5 10 15

5 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

10

15

20

25

30

35

40

45

50

55

EP 1 310 571 B1

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 5
 Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 10
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 15
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 20
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 25
 Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Asn Gly Gln
 145 150 155 160
 Pro Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
 165 170 175
 30
 Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
 180 185 190
 35
 Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
 195 200 205
 Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
 210 215 220
 40
 His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
 225 230 235 240
 45
 Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
 245 250 255
 Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
 260 265 270
 50
 Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
 275 280 285
 55

EP 1 310 571 B1

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
290 295 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305 310 315 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
325 330 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
340 345 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
355 360 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
370 375 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385 390 395 400

Thr Gly Asp Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
405 410 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
420 425 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
435 440 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
450 455 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465 470 475 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
485 490 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
500 505 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
515 520 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
530 535 540

EP 1 310 571 B1

5 Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
 545 550 555 560
 Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
 565 570 575
 10 Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
 580 585 590
 Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
 595 600 605
 15 Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
 610 615 620
 20 Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
 625 630 635 640
 Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
 645 650 655
 25 Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
 660 665 670
 30 Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
 675 680 685
 Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
 690 695 700
 35 Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
 705 710 715 720
 40 Thr Arg Tyr Leu Thr Arg Asn Leu
 725

<210> 104
 <211> 728
 <212> PRT
 <213> capsid protein of AAV serotype, clone 27.3VP1

<400> 104

50 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 55 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30

EP 1 310 571 B1

5

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

10

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

15

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

20

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Ser Gly Lys Lys Arg
130 135 140

25

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145 150 155 160

30

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
165 170 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
180 185 190

35

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
195 200 205

40

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
210 215 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225 230 235 240

45

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
245 250 255

50

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
260 265 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
275 280 285

55

EP 1 310 571 B1

5 Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
 290 295 300
 Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
 305 310 315 320
 10 Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
 325 330 335
 Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
 340 345 350
 15 Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
 355 360 365
 20 Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
 370 375 380
 Arg Ser Ser Phe Cys Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
 385 390 395 400
 25 Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
 405 410 415
 30 His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
 420 425 430
 Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
 435 440 445
 35 Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Val
 450 455 460
 40 Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
 465 470 475 480
 Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
 485 490 495
 45 Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
 500 505 510
 50 Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Leu
 515 520 525
 55 Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
 530 535 540

EP 1 310 571 B1

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545 550 555 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
565 570 575

Gln Ser Ser Thr Ala Gly Pro Arg Thr Gln Thr Val Asn Ser Gln Gly
580 585 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
595 600 605

Pro Ile Trp Ala Glu Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
610 615 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625 630 635 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
645 650 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
660 665 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
675 680 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
690 695 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705 710 715 720

Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 105

<211> 728

<212> PRT

<213> capsid protein of AAV serotype, clone 16.3VP1

<400> 105

EP 1 310 571 B1

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15

5 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30

10 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45

15

20

25

30

35

40

45

50

55

EP 1 310 571 B1

5
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60

10
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80

15
 Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95

20
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110

25
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125

30
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140

35
 Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
 145 150 155 160

40
 Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
 165 170 175

45
 Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
 180 185 190

50
 Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
 195 200 205

55
 Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
 210 215 220

60
 His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
 225 230 235 240

65
 Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
 245 250 255

70
 Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
 260 265 270

75
 Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
 275 280 285

80
 Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
 290 295 300

EP 1 310 571 B1

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
 305 310 315 320
 5
 Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
 325 330 335
 10
 Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
 340 345 350
 15
 Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
 355 360 365
 20
 Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Met Gly
 370 375 380
 25
 Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
 385 390 395 400
 Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
 405 410 415
 30
 His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
 420 425 430
 35
 Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
 435 440 445
 Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
 450 455 460
 40
 Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
 465 470 475 480
 Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
 485 490 495
 45
 Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
 500 505 510
 50
 Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Gly Gln Phe Phe
 515 520 525
 55
 Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
 530 535 540
 Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
 545 550 555 560

EP 1 310 571 B1

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
 565 570 575
 5
 Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
 580 585 590
 10
 Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
 595 600 605
 Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
 610 615 620
 15
 Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
 625 630 635 640
 20
 Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Gly Val Phe Thr Pro
 645 650 655
 Ala Leu Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
 660 665 670
 25
 Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
 675 680 685
 30
 Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
 690 695 700
 Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
 705 710 715 720
 35
 Thr Arg Tyr Leu Thr Arg Asn Leu
 725
 40
 <210> 106
 <211> 728
 <212> PRT
 <213> capsid protein of AAV serotype, clone 42.10
 45
 <400> 106
 50
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 55
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45

EP 1 310 571 B1

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 5
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 10
 Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 15
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 20
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Arg Lys Gly Gln
 145 150 155 160
 25
 Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
 165 170 175
 30
 Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
 180 185 190
 Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
 195 200 205
 35
 Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
 210 215 220
 40
 His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
 225 230 235 240
 Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
 245 250 255
 45
 Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
 260 265 270
 50
 Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
 275 280 285
 Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
 290 295 300

55

EP 1 310 571 B1

5 Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305 310 315 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
325 330 335

10 Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
340 345 350

15 Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
355 360 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
370 375 380

20 Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385 390 395 400

25 Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
405 410 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
420 425 430

30 Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
435 440 445

35 Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
450 455 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465 470 475 480

40 Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
485 490 495

45 Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
500 505 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
515 520 525

50 Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
530 535 540

55 Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545 550 555 560

EP 1 310 571 B1

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
 565 570 575
 5
 Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
 580 585 590
 10
 Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
 595 600 605
 Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
 610 615 620
 15
 Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
 625 630 635 640
 20
 Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
 645 650 655
 Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
 660 665 670
 25
 Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
 675 680 685
 30
 Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
 690 695 700
 Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
 705 710 715 720
 35
 Thr Arg Tyr Leu Thr Arg Asn Leu
 725

40 <210> 107
 <211> 728
 <212> PRT
 <213> capsid protein of AAV serotype, clone 42.3B
 45 <400> 107

50

55

EP 1 310 571 B1

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15

5 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30

10 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60

15

20

25

30

35

40

45

50

55

EP 1 310 571 B1

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

5
Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

10
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

15
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

20
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

25
Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145 150 155 160

30
Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
165 170 175

35
Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
180 185 190

40
Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
195 200 205

45
Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
210 215 220

50
His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225 230 235 240

55
Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
245 250 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
260 265 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
275 280 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
290 295 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305 310 315 320

EP 1 310 571 B1

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
 325 330 335
 5
 Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
 340 345 350
 10
 Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
 355 360 365
 Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
 370 375 380
 15
 Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
 385 390 395 400
 20
 Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
 405 410 415
 His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
 420 425 430
 25
 Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
 435 440 445
 Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
 450 455 460
 30
 Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
 465 470 475 480
 35
 Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Thr Ser Asn Phe Ala Trp
 485 490 495
 40
 Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
 500 505 510
 Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
 515 520 525
 45
 Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
 530 535 540
 50
 Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
 545 550 555 560
 55
 Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ser Ser Asn Leu
 565 570 575

EP 1 310 571 B1

5 Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
580 585 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
595 600 605

10 Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
610 615 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625 630 635 640

15 Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
645 650 655

20 Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
660 665 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
675 680 685

25 Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
690 695 700

30 Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705 710 715 720

Thr Arg Tyr Leu Thr Arg Asn Leu
725

35

<210> 108
<211> 728
<212> PRT
40 <213> capsid protein of AAV serotype, clone 42.11

<400> 108

45 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

50 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

55 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

EP 1 310 571 B1

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 5
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 10
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 15
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
 145 150 155 160
 20
 Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
 165 170 175
 25
 Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
 180 185 190
 Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
 195 200 205
 30
 Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
 210 215 220
 35
 His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
 225 230 235 240
 Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
 245 250 255
 40
 Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
 260 265 270
 45
 Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
 275 280 285
 Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
 290 295 300
 50
 Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
 305 310 315 320
 55

EP 1 310 571 B1

5
 Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
 325 330 335

10
 Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
 340 345 350

15
 Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
 355 360 365

20
 Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
 370 375 380

25
 Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
 385 390 395 400

30
 Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
 405 410 415

35
 His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
 420 425 430

40
 Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
 435 440 445

45
 Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
 450 455 460

50
 Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Arg Gln
 465 470 475 480

55
 Arg Leu Ser Lys Asp Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
 485 490 495

60
 Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
 500 505 510

65
 Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
 515 520 525

70
 Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
 530 535 540

75
 Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
 545 550 555 560

80
 Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
 565 570 575

EP 1 310 571 B1

5 Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
580 585 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
595 600 605

10 Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
610 615 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625 630 635 640

15 Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
645 650 655

20 Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
660 665 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
675 680 685

25 Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
690 695 700

30 Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705 710 715 720

Thr Arg Tyr Leu Thr Arg Asn Leu
725

35

<210> 109
<211> 729
<212> PRT
40 <213> capsid protein of AAV serotype, clone F1VP1

<400> 109

45 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

50 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

55 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

EP 1 310 571 B1

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95
 5
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 10
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 15
 Pro Ile Asp Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
 145 150 155 160
 Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
 165 170 175
 20
 Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
 180 185 190
 25
 Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
 195 200 205
 Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
 210 215 220
 30
 His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
 225 230 235 240
 35
 Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
 245 250 255
 Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr
 260 265 270
 40
 Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
 275 280 285
 45
 Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
 290 295 300
 50
 Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
 305 310 315 320
 Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
 325 330 335
 55

EP 1 310 571 B1

Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
340 345 350

5 Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
355 360 365

10 Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val
370 375 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385 390 395 400

15 Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro
405 410 415

20 Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
420 425 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr
435 440 445

25 Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr
450 455 460

30 Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln
465 470 475 480

Gln Gly Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala
485 490 495

35 Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr
500 505 510

40 Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe
515 520 525

Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn
530 535 540

45 Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys
545 550 555 560

50 Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn
565 570 575

Leu Gln Pro Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln
580 585 590

55

EP 1 310 571 B1

Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
 595 600 605
 5
 Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
 610 615 620
 10
 Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile
 625 630 635 640
 15
 Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr
 645 650 655
 Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
 660 665 670
 20
 Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
 675 680 685
 25
 Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val
 690 695 700
 Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile
 705 710 715 720
 30
 Gly Thr Arg Tyr Leu Pro Arg Asn Leu
 725

<210> 110

<211> 729

<212> PRT

<213> capsid protein of AAV serotype, clone F5VP1@3

<400> 110

EP 1 310 571 B1

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

5 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

10 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

15 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

20 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

EP 1 310 571 B1

5 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 10 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Ile Asp Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
 145 150 155 160
 15 Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
 165 170 175
 20 Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
 180 185 190
 Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Thr Ala
 195 200 205
 25 Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
 210 215 220
 30 His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
 225 230 235 240
 Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
 245 250 255
 35 Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr
 260 265 270
 40 Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
 275 280 285
 Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
 290 295 300
 45 Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
 305 310 315 320
 50 Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
 325 330 335
 55 Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
 340 345 350

EP 1 310 571 B1

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
 355 360 365
 5
 Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val
 370 375 380
 10
 Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
 385 390 395 400
 Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro
 405 410 415
 15
 Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
 420 425 430
 20
 Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr
 435 440 445
 Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr
 450 455 460
 25
 Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln
 465 470 475 480
 30
 Gln Arg Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala
 485 490 495
 Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr
 500 505 510
 35
 Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe
 515 520 525
 40
 Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn
 530 535 540
 Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys
 545 550 555 560
 45
 Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn
 565 570 575
 50
 Leu Gln Ser Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln
 580 585 590
 Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
 595 600 605
 55

EP 1 310 571 B1

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
 610 615 620
 5
 Ser Pro Leu Met Gly Gly Phe Gly Leu Glu His Pro Pro Pro Gln Ile
 625 630 635 640
 10
 Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr
 645 650 655
 Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
 660 665 670
 15
 Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
 675 680 685
 20
 Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val
 690 695 700
 Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile
 705 710 715 720
 25
 Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725

30 <210> 111
 <211> 729
 <212> PRT
 <213> capsid protein of AAV serotype, clone F3VP1

35 <400> 111

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15
 40
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30
 45
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 50
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 55
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
 85 90 95

EP 1 310 571 B1

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 5
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 10
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Ile Gly Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
 145 150 155 160
 15
 Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
 165 170 175
 20
 Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
 180 185 190
 Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
 195 200 205
 25
 Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
 210 215 220
 30
 His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
 225 230 235 240
 Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
 245 250 255
 35
 Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr
 260 265 270
 40
 Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
 275 280 285
 Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
 290 295 300
 45
 Pro Lys Lys Leu Arg Phe Lys Leu Leu Asn Ile Gln Val Lys Glu Val
 305 310 315 320
 50
 Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
 325 330 335
 Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
 340 345 350
 55

EP 1 310 571 B1

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
 355 360 365
 5
 Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asp Asn Gly Ser Gln Ser Val
 370 375 380
 10
 Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
 385 390 395 400
 Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro
 405 410 415
 15
 Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
 420 425 430
 20
 Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr
 435 440 445
 Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr
 450 455 460
 25
 Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln
 465 470 475 480
 30
 Gln Arg Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala
 485 490 495
 Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr
 500 505 510
 35
 Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe
 515 520 525
 40
 Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn
 530 535 540
 Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys
 545 550 555 560
 45
 Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn
 565 570 575
 50
 Leu Gln Ser Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln
 580 585 590
 Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
 595 600 605
 55

EP 1 310 571 B1

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
 610 615 620
 5
 Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile
 625 630 635 640
 10
 Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr
 645 650 655
 Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
 660 665 670
 15
 Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
 675 680 685
 20
 Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val
 690 695 700
 Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile
 705 710 715 720
 25
 Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725

30 <210> 112
 <211> 735
 <212> PRT
 <213> capsid protein of AAV serotype, clone 42.6B

35 <400> 112

40

45

50

55

EP 1 310 571 B1

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

5 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

10 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

15 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

20 Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

25

30

35

40

45

50

55

EP 1 310 571 B1

5 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 10 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 15 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 20 Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 25 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 30 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 35 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 40 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 45 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 50 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 55 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 60 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 65 Asn Asn Trp Gly Phe Arg Pro Arg Lys Leu Arg Phe Lys Leu Phe Asn
 305 310 315 320
 70 Ile Gln Val Lys Glu Val Thr Thr Asp Asp Gly Val Thr Thr Ile Ala
 325 330 335
 75 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln
 340 345 350
 80 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365

EP 1 310 571 B1

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

5 Asn Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

10 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
405 410 415

Thr Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

15 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

20 Ala Arg Thr Gln Ser Thr Thr Gly Ser Thr Arg Glu Leu Gln Phe His
450 455 460

Gln Ala Gly Pro Asn Thr Met Ala Glu Gln Ser Lys Asn Trp Leu Pro
465 470 475 480

25 Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Asn Ile Asp Ser Asn
485 490 495

30 Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
500 505 510

Gly Arg Asn Ser Leu Thr Asn Pro Gly Val Ala Met Ala Thr Asn Lys
515 520 525

35 Asp Asp Glu Asp Gln Phe Phe Pro Ile Asn Gly Val Leu Val Phe Gly
530 535 540

40 Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met Thr
545 550 555 560

Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr
565 570 575

45 Gly Val Val Ser Ser Asn Leu Gln Ser Ser Thr Ala Gly Pro Gln Thr
580 585 590

Gln Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn
595 600 605

50 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

55

EP 1 310 571 B1

Asp Gly Asn Phe His Pro Ser Pro Leu Met Asp Gly Phe Gly Leu Lys
625 630 635 640

5 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

10 Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

15 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

20 Ala Lys Ser Asn Asn Val Glu Phe Ala Val Asn Asn Glu Gly Val Tyr
705 710 715 720

Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

25
<210> 113
<211> 685
<212> PRT
<213> capsid protein of AAV serotype, clone 42.12
30
<400> 113

35 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

40 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

45 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

50 Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

55 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

EP 1 310 571 B1

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 5
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 10
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
 145 150 155 160
 Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
 165 170 175
 15
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
 180 185 190
 20
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
 195 200 205
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
 210 215 220
 25
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240
 30
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
 260 265 270
 35
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
 275 280 285
 40
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
 290 295 300
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
 305 310 315 320
 45
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
 325 330 335
 50
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
 340 345 350
 55
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
 355 360 365

EP 1 310 571 B1

	Pro	Ala	Asp	Val	Phe	Met	Ile	Pro	Gln	Tyr	Gly	Tyr	Leu	Thr	Leu	Asn
	370						375						380			
5																
	Asn	Gly	Ser	Gln	Ala	Val	Gly	Arg	Ser	Ser	Phe	Tyr	Cys	Leu	Glu	Tyr
	385					390					395					400
10																
	Phe	Pro	Ser	Gln	Met	Leu	Arg	Thr	Gly	Asn	Asn	Phe	Glu	Phe	Ser	Tyr
					405					410					415	
15																
	Gln	Phe	Glu	Asp	Val	Pro	Phe	His	Ser	Ser	Tyr	Ala	His	Ser	Gln	Ser
				420					425					430		
20																
	Leu	Asp	Arg	Leu	Thr	Asn	Pro	Leu	Ile	Asp	Gln	Tyr	Leu	Tyr	Tyr	Leu
			435					440					445			
25																
	Ala	Arg	Thr	Gln	Ser	Thr	Thr	Gly	Ser	Thr	Arg	Gly	Leu	Gln	Phe	His
		450					455					460				
30																
	Gln	Ala	Gly	Pro	Asn	Thr	Met	Ala	Glu	Gln	Ser	Lys	Asn	Trp	Leu	Pro
	465					470					475					480
35																
	Gly	Pro	Cys	Tyr	Arg	Gln	Gln	Arg	Leu	Ser	Lys	Asn	Ile	Asp	Ser	Asn
					485					490					495	
40																
	Asn	Asn	Ser	Asn	Phe	Ala	Trp	Thr	Gly	Ala	Thr	Lys	Tyr	His	Leu	Asn
				500					505					510		
45																
	Gly	Arg	Asn	Ser	Leu	Thr	Asn	Pro	Gly	Val	Ala	Met	Ala	Thr	Asn	Lys
			515					520					525			
50																
	Asp	Asp	Glu	Asp	Gln	Phe	Phe	Pro	Ile	Asn	Gly	Val	Leu	Val	Phe	Gly
		530					535					540				
55																
	Lys	Thr	Gly	Ala	Ala	Asn	Lys	Thr	Thr	Leu	Glu	Asn	Val	Leu	Met	Thr
	545					550					555					560
60																
	Ser	Glu	Glu	Glu	Ile	Lys	Thr	Thr	Asn	Pro	Val	Ala	Thr	Glu	Glu	Tyr
					565					570					575	
65																
	Gly	Val	Val	Ser	Ser	Asn	Leu	Gln	Ser	Ser	Thr	Ala	Gly	Pro	Gln	Thr
				580					585					590		
70																
	Gln	Thr	Val	Asn	Ser	Gln	Gly	Ala	Leu	Pro	Gly	Met	Val	Trp	Gln	Asn
			595					600								

EP 1 310 571 B1

Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

5 His Pro Pro Pro Gln Ile Leu Ile Lys Tyr Thr Ser Asn Tyr Tyr Lys
645 650 655

10 Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu
660 665 670

15 Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
675 680 685

<210> 114

<211> 724

<212> PRT

20 <213> capsid protein of AAV serotype, clone AAV5CAP

<400> 114

25

30

35

40

45

50

55

EP 1 310 571 B1

	Met	Ser	Phe	Val	Asp	His	Pro	Pro	Asp	Trp	Leu	Glu	Glu	Val	Gly	Glu	
	1				5					10					15		
5	Gly	Leu	Arg	Glu	Phe	Leu	Gly	Leu	Glu	Ala	Gly	Pro	Pro	Lys	Pro	Lys	
				20					25					30			
	Pro	Asn	Gln	Gln	His	Gln	Asp	Gln	Ala	Arg	Gly	Leu	Val	Leu	Pro	Gly	
10			35					40					45				
	Tyr	Asn	Tyr	Leu	Gly	Pro	Gly	Asn	Gly	Leu	Asp	Arg	Gly	Glu	Pro	Val	
		50					55					60					
15	Asn	Arg	Ala	Asp	Glu	Val	Ala	Arg	Glu	His	Asp	Ile	Ser	Tyr	Asn	Glu	
	65					70					75					80	
	Gln	Leu	Glu	Ala	Gly	Asp	Asn	Pro	Tyr	Leu	Lys	Tyr	Asn	His	Ala	Asp	
20					85					90					95		
	Ala	Glu	Phe	Gln	Glu	Lys	Leu	Ala	Asp	Asp	Thr	Ser	Phe	Gly	Gly	Asn	
				100					105					110			
25	Leu	Gly	Lys	Ala	Val	Phe	Gln	Ala	Lys	Lys	Arg	Val	Leu	Glu	Pro	Phe	
			115					120					125				
	Gly	Leu	Val	Glu	Glu	Gly	Ala	Lys	Thr	Ala	Pro	Thr	Gly	Lys	Arg	Ile	
30		130					135					140					
	Asp	Asp	His	Phe	Pro	Lys	Arg	Lys	Lys	Ala	Arg	Thr	Glu	Glu	Asp	Ser	
	145					150					155					160	
35	Lys	Pro	Ser	Thr	Ser	Ser	Asp	Ala	Glu	Ala	Gly	Pro	Ser	Gly	Ser	Gln	
					165					170					175		

EP 1 310 571 B1

5

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
180 185 190

10

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
195 200 205

15

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
210 215 220

20

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225 230 235 240

25

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
245 250 255

30

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
260 265 270

35

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
275 280 285

40

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
290 295 300

45

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305 310 315 320

50

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
325 330 335

55

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
340 345 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
355 360 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
370 375 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385 390 395 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
405 410 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
420 425 430

EP 1 310 571 B1

5
 Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
 435 440 445

10
 Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
 450 455 460

15
 Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
 465 470 475 480

20
 Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
 485 490 495

25
 Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
 500 505 510

30
 Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
 515 520 525

35
 Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
 530 535 540

40
 Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
 545 550 555 560

45
 Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
 565 570 575

50
 Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
 580 585 590

55
 Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
 595 600 605

60
 Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
 610 615 620

65
 Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
 625 630 635 640

70
 Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
 645 650 655

75
 Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
 660 665 670

80
 Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
 675 680 685

EP 1 310 571 B1

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

5

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

10

<210> 115

<211> 9

15

<212> DNA

<213> DraIII restriction enzyme site

<400> 115

20

caccacgtc

9

<210> 116

25

<211> 28

<212> DNA

<213> AV2cas

<400> 116

30

cgcagagacc aaagttcaac tgaaacga

28

35

<210> 117

<211> 255

<212> DNA

<213> adeno-associated virus serotype 10

40

<400> 117

ggtaattcct ccggaaattg gcattgcgat tccacatggc tgggcgacag agtcatcacc 60

45

accagcaccc gaacctgggt cctgcccacc tacaacaacc acatctacaa gcaaattctcc 120

agcgagacag gagccaccaa cgacaaccac tacttctggct acagcacccc ctggggggtat 180

tttgacttta acagattcca ctgccacttt tcaccacgtg actggcagcg actcatcaac 240

50

aacaactggg gattc 255

55

<210> 118

<211> 258

<212> DNA

<213> adeno-associated virus serotype 11

EP 1 310 571 B1

<400> 118

	ggtaattcct ccggaaattg gcattgcat tccacatggc tgggcgacag agtcattacc	60
5	accagcaccg gaacctgggc cctgccaacc tacaacaacc acctctacaa acaaattctcc	120
	agcgcttcaa cggggggccag caacgacaac cactactttg gctacagcac cccctggggg	180
10	tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcacc	240
	aacaacaact ggggattc	258

15 <210> 119
 <211> 255
 <212> DNA
 <213> adeno-associated virus serotype 12

20 <400> 119

	ggtaattcct ccggaaattg gcattgcat tccacatggc tgggcgaccg agtcattacc	60
25	accagcaccg ggacttgggc cctgcccacc tacaacaacc acctctacaa gcaaattctcc	120
	agccaatcgg gtgccaccaa cgacaaccac tacttcggct acagcaccg ttgggggtat	180
	tttgatttca acagattcca ctgccatttc tcaccacgtg actggcagcg actcatcaac	240
30	aacaactggg gattc	255

35 <210> 120
 <211> 2205
 <212> DNA
 <213> adeno-associated virus serotype, clone A3.1vp1
 <400> 120

40

45

50

55

EP 1 310 571 B1

atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaatcaga 60
 cagtgggtgga agctcaaacc tggcccacca ccgccgaaac ctaaccaaca acaccgggac 120
 5 gacagtaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
 aaaggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
 caccagctca agcaagggga caaccgtac ctcaaataca accacgcgga cgctgaattt 300
 10 caggagcgtc ttcaagaaga tacgtctttc gggggcaacc tcgggcgagc agtcttccag 360
 gccaaaaaga ggggtactga gcctcttggg ctggttgagg aagctgttaa gacggctcct 420
 ggaaaaaaga gacctataga gcagtctcct gcagaaccgg actcttcctc gggcatcggc 480
 15 aaatcaggcc agcagcccg ctaagaaaaga ctcaattttg gtcagactgg cgacacagag 540
 tcagtcccag accctcaacc aatcggagaa ccccccgcag cccctcttg tgtgggatct 600
 aatacaatgg cttcaggcgg tggggcacca atggcagaca ataacgaagg cgccgacgga 660
 20 gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagttatc 720
 accaccagca caagaacctg ggccctcccc acctacaata atcacctcta caagcaaata 780
 tccagcgaat cgggagccac caacgacaac cactacttcg gctacagcac cccctggggg 840
 25 tattttgact ttaacagatt ccactgtcac ttctcaccac gtgactggca gcgactcatc 900
 aacaacaact ggggatttag acccaagaaa ctcaatttca agctcttcaa catccaagtc 960
 aaggaggtca cgcagaatga tggaaccacg accatcgcca ataaccttac cagcacggtg 1020
 30
 35
 40
 45
 50
 55

5 caggtcttca cagactctga gtaccagctg ccctacgtcc tcggttcggc tcaccagggc 1080
 tgccttccgc cgttcccagc agacgtcttc atgattcctc agtacggcta cttgactctg 1140
 aacaatggca gccaagcggg aggacgttct tcattctact gtctagagta ttttccctct 1200
 cagatgctga ggacgggaaa caacttcacc ttcagctaca cttttgaaga cgtgcctttc 1260
 10 cacagcagct acgcgcacag ccagagtctg gatcggctga tgaatcctct cattgaccag 1320
 tacctgtatt acctgagcaa aactcagggt acaagtggaa caacgcagca atcgagactg 1380
 cagttcagcc aagctgggccc tagctccatg gctcagcagg ccaaaaactg gctaccggga 1440
 15 cccagctacc gacagcagcg aatgtctaag acggctaata acaacaacaa cagtgaattt 1500
 gcttggactg cagccaccaa atattacctg aatggaagaa attctctggt caatcccggg 1560
 cccccaatgg ccagtcacaa ggacgatgag gaaaagtatt tccccatgca cggaaatctc 1620
 20 atcttttgaa aacaaggcac aggaactacc aatgtggaca ttgaatcagt gcttattaca 1680
 gacgaagaag aaatcagaac aactaatcct gtggctacag aacaatacgg acaggttgcc 1740
 accaaccatc agagtcagaa caccacagct tcctatggaa gtgtggacag ccagggaatc 1800
 25 ttacctggaa tgggtgtggca ggaccgcgat gtctatcttc aagggtcccat ttgggcaaaa 1860
 actcctcaca cggacggaca ctttcatcct tctccgctca tgggaggctt tggactgaaa 1920
 caccctcctc cccagatcct gatcaaaaac acacctgtgc cagcgaatcc cgcgaccact 1980
 30 ttcactcctg gaaagtttgc ttcgttcatt acccagtatt ccaccggaca ggtagcgtg 2040
 gaaatagagt gggagctgca gaaagaaaac agcaaagcgt ggaaccaga aattcagtac 2100
 acctccaact acaacaagtc ggtgaatgtg gagtttaccg tggacgcaaa cgggtgtttat 2160
 35 tctgaacccc gccctattgg cactcgttac cttaccggga acttg 2205

40 Claims

1. A method of identifying unknown adeno-associated virus (AAV) sequences in a sample suspected of containing AAV from a latent infection, said method comprising the steps of:

45 (a) subjecting the sample containing DNA to amplification via polymerase chain reaction (PCR) using a first set of primers which specifically amplify a first AAV region comprising at least 250 bp of AAV capsid nucleic acid sequences, said first region having a variable sequence flanked by at least 18 base pairs of highly conserved sequence at its 5' end and at least 18 base pairs of highly conserved sequence at its 3' end, said base pairs being highly conserved relative to an alignment of at least AAV1, AAV2, AAV3, AAV4, AAV5 and AAV6;
 50 (b) optionally subjecting the DNA to further amplification using a second set of primers which specifically amplify a second region which comprises the first region of AAV sequences and sequences which are 5' to the first region, such that AAV 5' extension sequences which anneal to the 5' end of the AAV sequences amplified by the primers for the first region are obtained;
 55 (c) optionally subjecting the DNA to further amplification using a third set of primers which specifically amplify a third region which comprises the first region of AAV sequences and sequences which are 3' to the first region, such that AAV 3' extension sequences which anneal to the 3' end of the AAV sequences amplified by the primers for the first region are obtained,

each of said second and third regions being predetermined based upon the alignment of the nucleic acid sequences of at least AAV1, AAV2, AAV3, AAV4, AAV5 and AAV6, and each of said regions comprising nucleic acid sequences which are highly conserved over at least 18 base pairs at the 5' end, optionally variable sequences in the middle, and sequences which are highly conserved over at least 18 base pairs at the 3' end of the sequences of the region, relative to the sequences of at least AAV1, AAV2, AAV3, AAV4, AAV5 and AAV6; and each of the sets of primers consisting of a 5' primer and a 3' primer; the presence of amplified sequences indicating the presence of an AAV in the sample, and a comparison of differences between the amplified sequences and the sequences of AAV1, AAV2, AAV3, AAV4, AAV5 and AAV6 indicating the presence of an unknown AAV.

2. A method according to claim 1, wherein the comparison comprises the step of comparing restriction enzyme patterns for the amplified sequences to restriction enzyme patterns of AAV1, AAV2, AAV3, AAV4, AAV5 and AAV6.
3. A method according to claim 1 or claim 2, wherein step (a) amplifies the full-length capsid gene.
4. A method according to any of claims 1 to 3, wherein the amplified sequences comprise the AAV capsid gene and the AAV rep gene.
5. A method according to any of claims 1 to 4, wherein the DNA has been extracted from cells, cell culture, tissue, tissue culture or biological fluids.
6. A method according to any of claims 1 to 5, wherein the first region is highly conserved over at least about 25 base pairs at the 5' end of the region, the 3' end of the region or both.
7. A method according to claim 6, wherein the first region is highly conserved over at least about 30 base pairs at the 5' end of the region, the 3' end of the region or both.
8. A method according to any of claims 1 to 7, wherein the highly conserved sequences of the first region have at least 80% identity among the aligned AAVs at the 5' end of the region, the 3' end of the region or both.
9. A method according to claim 8, wherein the highly conserved sequences of the first region have at least 90% identity among the aligned AAVs at the 5' end of the region, the 3' end of the region or both.
10. A method according to any of claims 1 to 9, wherein the variable sequences in the middle of the first region have less than 70% identity among the aligned AAVs.
11. A method according to any of claims 1 to 10, wherein the first region spans about bp 2800 to about 3200 of AAV 1, SEQ ID NO:6, and corresponding base pairs in other AAVs.
12. A method according to claim 11, wherein the first region is 257 bp spanning bp 2886 to about 3143 of AAV 1, SEQ ID NO:6, and corresponding base pairs in other AAVs.
13. A method according to any of claims 1 to 5, wherein the primers are AV1ns, having the sequence of nucleotides 1398 to 1423 of SEQ ID NO:6, and AV2cas, having the sequence of SEQ ID NO:7.
14. A method according to claim 1 or claim 2, wherein the first set of primers allows isolation of full-length adeno-associated virus capsid sequences from a sample, the first set of primers comprising a 5' primer directed to a region located in the middle of an AAV rep gene, based on a predetermined conserved region, and a 3' primer directed to a region downstream of an AAV cap gene, based on a predetermined conserved region of AAV.
15. A method according to any of claims 1 to 14, wherein the sample comprises AAV integrated into the chromosome.
16. A method according to any of claims 1 to 15, wherein the sample comprises human tissue.
17. A method according to any of claims 1 to 16, wherein the sample contains proviral AAV sequences.
18. A method according to any of claims 1 to 17, wherein the first region is a signature region.

19. A method according to any of claims 1 to 18, wherein the base pairs of the highly conserved sequences are highly conserved relative to an alignment of AAVs 1,2,3,4,5 and 6 and AAVs isolated from geese and ducks.
20. A method according to any of claims 1 to 19, wherein the variable sequence is a hypervariable sequence.
21. A method according to any of claims 1 to 20, wherein the first region comprises up to 10 kilobasepairs in length.
22. A method according to claim 21, wherein the first region comprises a 3-1 kilobase pair fragment comprising the full-length cap sequence.
23. A kit for detecting the presence of an unknown adeno-associated virus (AAV) in a sample from cellular DNA suspected of containing a latent AAV infection, said kit comprising:
 - (a) a first set of primers which specifically amplify a first region comprising 250 bp of AAV capsid nucleic acid sequences, said first region having at least 18 base pairs of highly conserved sequence at its 5' end, a variable sequence, and at least 18 base pairs of highly conserved sequence at its 3' end, said base pairs being highly conserved relative to an alignment of at least AAV1, AAV2, AAV3, AAV4, AAV5 and AAV6;
 - (b) optionally a second set of primers specific for a second region of the AAV nucleic acid sequences which comprises the first region of AAV sequences and sequences which are 5' to the first region, such that AAV 5' extension sequences which anneal to the 5' end of the AAV sequences amplified by the primers for the first region are obtained;
 - (c) optionally a third set of primers which specifically amplify a third region which comprises the first region of AAV sequences and sequences which are 3' to the first region, such that AAV 3' extension sequences which anneal to the 3' end of the AAV sequences amplified by the primers for the first region are obtained;each of said second and third regions being predetermined based upon the alignment of the nucleic acid sequences of at least AAV1, AAV2, AAV3, AAV4, AAV5 and AAV6, and each of said regions comprising nucleic acid sequences which are highly conserved over at least 18 base pairs at the 5' end, optionally variable sequences in the middle, and sequences which are highly conserved over at least 18 base pairs at the 3' end of the sequences of the region, relative to the sequences of at least AAV1, AAV2, AAV3, AAV4, AAV5 and AAV6;each of the sets of primers consisting of a 5' primer and a 3' primer, each of said primers comprising at least 15 nucleotides complementary to its respective highly conserved sequence and having exact identity with its respective highly conserved sequence over at least 5 base pairs in its 3' end.
24. A kit according to claim 23, wherein the 5' primer and/or the 3' primer comprises at least 18 nucleotides.
25. A kit according to claim 24, wherein the 5' primer and/or the 3' primer comprises 25 nucleotides.
26. A kit according to any of claims 23 to 25, wherein the 5' primer and/or the 3' primer comprises at least 9 base pairs of exact identity at its 3' end.
27. A kit according to claim 26, wherein the 5' primer and/or the 3' primer comprises at least 18 base pairs of exact identity at its 3' end.
28. A kit according to any of claims 23 to 27, wherein the first set of primers allows isolation of full-length adeno-associated virus capsid sequences from a sample, the first set of primers comprising a 5' primer directed to a region located in the middle of an AAV rep gene, based on a predetermined conserved region of AAV, and a 3' primer directed to a region downstream of an AAV cap gene, based on a predetermined conserved region of AAV.
29. A kit according to claim 23, wherein the 5' primer has a sequence comprising GCTGCGTCAACTGGACCAATGA-GAAC, which corresponds to nt 1398 to 1423 of SEQ ID NO:6.
30. A kit according to claim 23, wherein the 3' primer has a sequence comprising CGCAGAGACCAAAGTTCAACT-GAAACGA, which corresponds to the nucleotides complementary to 4462-4435 of SEQ ID NO:7.
31. A kit according to any of claims 23 to 30, wherein the sample comprises AAV integrated into the chromosome.

Patentansprüche

1. Verfahren zur Identifizierung unbekannter Sequenzen von adeno-assoziiertem Virus (AAV) in einer Probe, von der man annimmt, daß sie von einer latenten Infektion herrührendes AAV enthält, wobei man in den folgenden Verfahrensschritten

(a) die DNA-haltige Probe einer Amplifikation über eine Polymerasekettenreaktion (PCR) unter Verwendung eines ersten Primersatzes, mit dem spezifisch ein mindestens 250 Bp AAV-Capsid-Nukleinsäuresequenzen umfassender erster AAV-Bereich amplifiziert wird, wobei dieser erste Bereich eine an ihrem 5'-Ende von mindestens 18 Basenpaaren hochkonservierter Sequenz und an ihrem 3'-Ende von mindestens 18 Basenpaaren hochkonservierter Sequenz flankierte variable Sequenz aufweist, wobei die Basenpaare relativ zu einer vergleichenden Anordnung von mindestens AAV1, AAV2, AAV3, AAV4, AAV5 und AAV6 hochkonserviert sind, aussetzt,

(b) gegebenenfalls die DNA einer weiteren Amplifikation unter Verwendung eines zweiten Primersatzes, mit dem spezifisch ein zweiter Bereich, der den ersten Bereich von AAV-Sequenzen sowie 5' zum ersten Bereich liegende Sequenzen umfaßt, amplifiziert wird, aussetzt, so daß 5'-AAV-Verlängerungssequenzen, die in einer Annealing-Reaktion an das 5'-Ende der mit den Primern für den ersten Bereich amplifizierten AAV-Sequenzen binden, erhalten werden,

(c) gegebenenfalls die DNA einer weiteren Amplifikation unter Verwendung eines dritten Primersatzes, mit dem spezifisch ein dritter Bereich, der den ersten Bereich von AAV-Sequenzen sowie 3' zum ersten Bereich liegende Sequenzen umfaßt, amplifiziert wird, aussetzt, so daß 3'-AAV-Verlängerungssequenzen, die in einer Annealing-Reaktion an das 3'-Ende der mit den Primern für den ersten Bereich amplifizierten AAV-Sequenzen binden, erhalten werden,

wobei der zweite und der dritte Bereich jeweils auf der Grundlage der vergleichenden Anordnung der Nukleinsäuresequenzen von mindestens AAV1, AAV2, AAV3, AAV4, AAV5 und AAV6 vorbestimmt sind und die Bereiche relativ zu den Sequenzen von mindestens AAV1, AAV2, AAV3, AAV4, AAV5 und AAV6 jeweils am 5'-Ende der Sequenzen des Bereichs über mindestens 18 Basenpaare hochkonservierte Nukleinsäuresequenzen, in der Mitte gegebenenfalls variable Sequenzen und am 3'-Ende über mindestens 18 Basenpaare hochkonservierte Sequenzen umfassen und

die Primersätze jeweils aus einem 5'-Primer und einem 3'-Primer bestehen, das Vorhandensein amplifizierter Sequenzen das Vorhandensein eines AAV in der Probe anzeigt, und ein Vergleich der Unterschiede zwischen den amplifizierten Sequenzen und den Sequenzen von AAV1, AAV2, AAV3, AAV4, AAV5 und AAV6 das Vorhandensein eines unbekannten AAV anzeigt.

2. Verfahren nach Anspruch 1, wobei der Vergleich den Schritt des Vergleichens von Restriktionsenzymmustern für die amplifizierten Sequenzen mit Restriktionsenzymmustern von AAV1, AAV2, AAV3, AAV4, AAV5 und AAV6 umfaßt.
3. Verfahren nach Anspruch 1 oder 2, wobei in Schritt (a) das Capsid-Gen in voller Länge amplifiziert wird.
4. Verfahren nach einem der Ansprüche 1 bis 3, wobei die amplifizierten Sequenzen das AAV-Capsid-Gen und das AAV-rep-Gen umfassen.
5. Verfahren nach einem der Ansprüche 1 bis 4, wobei die DNA aus Zellen, Zellkultur, Gewebe, Gewebekultur oder biologischen Flüssigkeiten extrahiert wurde.
6. Verfahren nach einem der Ansprüche 1 bis 5, wobei der erste Bereich über mindestens etwa 25 Basenpaare am 5'-Ende oder/und am 3'-Ende des Bereichs hochkonserviert ist.
7. Verfahren nach Anspruch 6, wobei der erste Bereich über mindestens etwa 30 Basenpaare am 5'-Ende oder/und am 3'-Ende des Bereichs hochkonserviert ist.
8. Verfahren nach einem der Ansprüche 1 bis 7, wobei die hochkonservierten Sequenzen des ersten Bereichs unter den vergleichend angeordneten AAVs eine Identität von mindestens 80% am 5'-Ende oder/und am 3'-Ende des Bereichs aufweisen.
9. Verfahren nach Anspruch 8, wobei die hochkonservierten Sequenzen des ersten Bereichs unter den vergleichend

angeordneten AAVs eine Identität von mindestens 90% am 5'-Ende oder/und am 3'-Ende des Bereichs aufweisen.

10. Verfahren nach einem der Ansprüche 1 bis 9, wobei die variablen Sequenzen in der Mitte des ersten Bereichs unter den vergleichend angeordneten AAVs eine Identität von weniger als 70% aufweisen.

11. Verfahren nach einem der Ansprüche 1 bis 10, wobei der erste Bereich von etwa Bp 2800 bis etwa 3200 von AAV1, SEQ ID NO:6, und den entsprechenden Basenpaaren in anderen AAV reicht.

12. Verfahren nach Anspruch 11, wobei es sich bei dem ersten Bereich um 257 Bp handelt, die von Bp 2886 bis etwa 3143 von AAV1, SEQ ID NO:6, und den entsprechenden Basenpaaren in anderen AAV reichen.

13. Verfahren nach einem der Ansprüche 1 bis 5, wobei es sich bei den Primern um AV1ns mit der Sequenz der Nukleotide 1398 bis 1423 der SEQ ID NO:6 sowie um AV2cas mit der Sequenz der SEQ ID NO:7 handelt.

14. Verfahren nach Anspruch 1 oder Anspruch 2, wobei der erste Primersatz die Isolierung von Capsidsequenzen in voller Länge von adeno-assoziiertem Virus aus einer Probe gestattet, wobei der erste Primersatz einen auf einen in der Mitte eines AAV-rep-Gens liegenden Bereich auf der Grundlage eines vorbestimmten konservierten Bereichs gerichteten 5'-Primer sowie einen auf einen stromabwärts von einem AAV-cap-Gen liegenden Bereich auf der Grundlage eines vorbestimmten konservierten Bereichs von AAV gerichteten 3'-Primer umfaßt.

15. Verfahren nach einem der Ansprüche 1 bis 14, wobei die Probe in das Chromosom integriertes AAV umfaßt.

16. Verfahren nach einem der Ansprüche 1 bis 15, wobei die Probe menschliches Gewebe umfaßt.

17. Verfahren nach einem der Ansprüche 1 bis 16, wobei die Probe provirale AAV-Sequenzen enthält.

18. Verfahren nach einem der Ansprüche 1 bis 17, wobei es sich bei dem ersten Bereich um einen Signaturbereich handelt.

19. Verfahren nach einem der Ansprüche 1 bis 18, wobei die Basenpaare der hochkonservierten Sequenzen relativ zu einer vergleichenden Anordnung von AAV 1, 2, 3, 4, 5 und 6 und aus Gans und Ente isolierten AAV hochkonserviert sind.

20. Verfahren nach einem der Ansprüche 1 bis 19, wobei es sich bei der variablen Sequenz um eine hypervariable Sequenz handelt.

21. Verfahren nach einem der Ansprüche 1 bis 20, wobei der erste Bereich eine Länge von bis zu 10 Kilobasenpaaren umfaßt.

22. Verfahren nach Anspruch 21, wobei der erste Bereich ein die cap-Sequenz in voller Länge umfassendes Fragment von 3,1 Kilobasenpaaren umfaßt.

23. Kit zum Nachweis des Vorhandenseins eines unbekannten adeno-assoziierten Virus (AAV) in einer Probe aus zellulärer DNA, von der man annimmt, daß sie eine latente AAV-Infektion enthält, wobei der Kit umfaßt:

(a) einen ersten Primersatz, mit dem spezifisch ein 250 Bp AAV-Capsid-Nukleinsäuresequenzen umfassender erster AAV-Bereich amplifiziert wird, wobei dieser erste Bereich an seinem 5'-Ende mindestens 18 Basenpaare hochkonservierter Sequenz, eine variable Sequenz und an seinem 3'-Ende mindestens 18 Basenpaare hochkonservierter Sequenz aufweist, wobei die Basenpaare relativ zu einer vergleichenden Anordnung von mindestens AAV1, AAV2, AAV3, AAV4, AAV5 und AAV6 hochkonserviert sind,

(b) gegebenenfalls einen für einen zweiten Bereich der AAV-Nukleinsäuresequenzen, der den ersten Bereich von AAV-Sequenzen sowie 5' zum ersten Bereich liegende Sequenzen umfaßt, spezifischen zweiten Primersatz, so daß 5'-AAV-Verlängerungssequenzen, die in einer Annealing-Reaktion an das 5'-Ende der mit den Primern für den ersten Bereich amplifizierten AAV-Sequenzen binden, erhalten werden,

(c) gegebenenfalls einen dritten Primersatz, mit dem spezifisch ein dritter Bereich, der den ersten Bereich von AAV-Sequenzen sowie 3' zum ersten Bereich liegende Sequenzen umfaßt, amplifiziert wird, so daß 3'-AAV-Verlängerungssequenzen, die in einer Annealing-Reaktion an das 3'-Ende der mit den Primern für den ersten

Bereich amplifizierten AAV-Sequenzen binden, erhalten werden,

wobei der zweite und der dritte Bereich jeweils auf der Grundlage der vergleichenden Anordnung der Nukleinsäuresequenzen von mindestens AAV1, AAV2, AAV3, AAV4, AAV5 und AAV6 vorbestimmt sind und die Bereiche relativ zu den Sequenzen von mindestens AAV1, AAV2, AAV3, AAV4, AAV5 und AAV6 jeweils am 5'-Ende der Sequenzen des Bereichs über mindestens 18 Basenpaare hochkonservierte Nukleinsäuresequenzen, in der Mitte gegebenenfalls variable Sequenzen und am 3'-Ende über mindestens 18 Basenpaare hochkonservierte Sequenzen umfassen,

die Primersätze jeweils aus einem 5'-Primer und einem 3'-Primer bestehen, wobei jeder Primer mindestens 15 zur hochkonservierten Sequenz des jeweils anderen Primers komplementäre Nukleotide umfaßt und an seinem 3'-Ende über mindestens 5 Basenpaare eine genaue Identität mit der hochkonservierten Sequenz des jeweils anderen Primers aufweist.

24. Kit nach Anspruch 23, wobei der 5'-Primer und/oder der 3'-Primer mindestens 18 Nukleotide umfaßt.

25. Kit nach Anspruch 24, wobei der 5'-Primer und/oder der 3'-Primer mindestens 25 Nukleotide umfaßt.

26. Kit nach einem der Ansprüche 23 bis 25, wobei der 5'-Primer und/oder der 3'-Primer an seinem 3'-Ende mindestens 9 Basenpaare genauer Identität umfaßt.

27. Kit nach Anspruch 26, wobei der 5'-Primer und/oder der 3'-Primer an seinem 3'-Ende mindestens 18 Basenpaare genauer Identität umfaßt.

28. Kit nach einem der Ansprüche 23 bis 27, wobei der erste Primersatz die Isolierung von Capsidsequenzen in voller Länge von adeno-assoziiertem Virus aus einer Probe gestattet, wobei der erste Primersatz einen auf einen in der Mitte eines AAV-rep-Gens liegenden Bereich auf der Grundlage eines vorbestimmten konservierten Bereichs von AAV gerichteten 5'-Primer sowie einen auf einen stromabwärts von einem AAV-cap-Gen liegenden Bereich auf der Grundlage eines vorbestimmten konservierten Bereichs von AAV gerichteten 5'-Primer umfaßt.

29. Kit nach Anspruch 23, wobei der 5'-Primer eine GCTGCGTCAACTGGACCAATGAGAAC umfassende Sequenz aufweist, die Nt 1398 bis 1423 der SEQ ID NO:6 entspricht.

30. Kit nach Anspruch 23, wobei der 3'-Primer eine CGCAGAGACCAAAGTTCAACTGAAACGA umfassende Sequenz aufweist, die den zu 4462-4435 der SEQ ID NO:7 komplementären Nukleotiden entspricht.

31. Kit nach einem der Ansprüche 23 bis 30, wobei die Probe in das Chromosom integriertes AAV umfaßt.

Revendications

1. Procédé pour identifier des séquences de virus associés à l'adénovirus (VAA) inconnus dans un échantillon dont on suspecte qu'il contient des VAA provenant d'une infection latente, ledit procédé comprenant les étapes :

(a) de soumission de l'échantillon contenant l'ADN à une amplification via une réaction de polymérase en chaîne (PCR) en utilisant une première série d'amorces qui amplifient spécifiquement une première région de VAA comprenant au moins 250 pb des séquences d'acides nucléiques de capsid de VAA, ladite première région présentant une séquence variable adjacente à au moins 18 paires de bases d'une séquence hautement conservée en son extrémité 5' et à au moins 18 paires de bases d'une séquence hautement conservée en son extrémité 3', lesdites paires de bases étant hautement conservées par rapport à un alignement d'au moins VAA1, VAA2, VAA3, VAA4, VAA5 et VAA6;

(b) éventuellement de soumission de l'ADN à une autre amplification en utilisant une deuxième série d'amorces qui amplifient spécifiquement une deuxième région qui comprend la première région de séquences des VAA et des séquences qui sont côté 5' par rapport à la première région, de telle manière qu'on obtient des séquences d'extension 5' de VAA qui hybrident sur l'extrémité 5' des séquences de VAA amplifiées par les amorces pour la première région ;

(c) éventuellement de soumission de l'ADN à une autre amplification utilisant une troisième série d'amorces qui amplifient spécifiquement une troisième région qui comprend la première région de séquences de VAA et

les séquences qui sont situées côté 3' par rapport à la première région, de telle manière qu'on obtient des séquences d'extension 3' de VAA qui hybrident sur l'extrémité 3' des séquences de VAA amplifiées par les amorces pour la première région,

- 5
10
15
20
25
30
35
40
45
50
55
- chacune desdites deuxième et troisième régions étant prédéterminée sur base de l'alignement des séquences d'acides nucléiques d'au moins VAA1, VAA2, VAA3, VAA4, VAA5 et VAA6, et chacune desdites régions comprenant des séquences d'acides nucléiques qui sont hautement conservées sur au moins 18 paires de bases en l'extrémité 5', des séquences éventuellement variables au centre et des séquences qui sont hautement conservées sur au moins 18 paires de bases en l'extrémité 3' des séquences de la région, par rapport aux séquences d'au moins VAA1, VAA2, VAA3, VAA4, VAA5 et VAA6; et
- chacune des séries d'amorces étant constituée par une amorce 5' et une amorce 3';
- la présence de séquences amplifiées indiquant la présence d'un VAA dans l'échantillon et
- une comparaison des différences entre les séquences amplifiées et les séquences des VAA1, VAA2, VAA3, VAA4, VAA5 et VAA6 indiquant la présence d'un VAA inconnu.
2. Procédé selon la revendication 1, dans lequel la comparaison comprend l'étape de comparaison de modèles d'enzymes de restriction pour les séquences amplifiées à des modèles d'enzymes de restriction des VAA1, VAA2, VAA3, VAA4, VAA5 et VAA6.
3. Procédé selon la revendication 1 ou 2, dans lequel l'étape (a) amplifie toute la longueur du gène cap.
4. Procédé selon l'une quelconque des revendications 1 à 3, dans lequel les séquences amplifiées comprennent le gène cap du VAA et le gène rep du VAA.
5. Procédé selon l'une quelconque des revendications 1 à 4, dans lequel l'ADN a été extrait de cellules, d'une culture cellulaire, de tissu, d'une culture de tissu ou de fluides biologiques.
6. Procédé selon l'une quelconque des revendications 1 à 5, dans lequel la première région est hautement conservée sur au moins 25 paires de base en l'extrémité 5' de la région, en l'extrémité 3' de la région ou les deux.
7. Procédé selon la revendication 6, dans lequel la première région est hautement conservée sur au moins 30 paires de base en l'extrémité 5' de la région, en l'extrémité 3' de la région ou les deux.
8. Procédé selon l'une quelconque des revendications 1 à 7, dans lequel les séquences hautement conservées de la première région présentent une identité d'au moins 80% avec les VAA alignés en l'extrémité 5' de la région, l'extrémité 3' de la région ou les deux.
9. Procédé selon la revendication 8, dans lequel les séquences hautement conservées de la première région présentent une identité d'au moins 90% avec les VAA alignés en l'extrémité 5' de la région, l'extrémité 3' de la région ou les deux.
10. Procédé selon l'une quelconque des revendications 1 à 9, dans lequel les séquences variables au centre de la première région présentent une identité inférieure à 70% avec les VAA alignés.
11. Procédé selon l'une quelconque des revendications 1 à 10, dans lequel la première région s'étend de la paire de bases 2800 à environ 3200 du VAA 1, SEQ ID NO:6, et les paires de bases correspondantes dans les autres VAA.
12. Procédé selon la revendication 11, dans lequel la première région représente 257 paires de bases, s'étendant de la paire de bases 2886 à environ 3143 du VAA1, SEQ ID NO:6, et les paires de bases correspondantes dans les autres VAA.
13. Procédé selon l'une quelconque des revendications 1 à 5, dans lequel les amorces sont des AV1ns, présentant la séquence des nucléotides 1398 à 1423 de la SEQ ID NO:6, et des AV2cas, présentant la séquence de la SEQ ID NO:7.
14. Procédé selon la revendication 1 ou 2, dans lequel la première série d'amorces permet l'isolement de toute la longueur de séquences de capsid du virus associé à l'adénovirus d'un échantillon, la première série d'amorces comprenant une amorce 5' dirigée sur une région localisée au centre d'un gène rep du VAA, sur base d'une région prédéterminée conservée et une amorce 3', dirigée sur une région en aval d'un gène cap du VAA, basée sur une

région prédéterminée conservée du VAA.

15. Procédé selon l'une quelconque des revendications 1 à 14, dans lequel l'échantillon comprend un VAA intégré dans le chromosome.

16. Procédé selon l'une quelconque des revendications 1 à 15, dans lequel l'échantillon comprend du tissu humain.

17. Procédé selon l'une quelconque des revendications 1 à 16, dans lequel l'échantillon contient des séquences de VAA provirales.

18. Procédé selon l'une quelconque des revendications 1 à 17, dans lequel la première région est une région de signature.

19. Procédé selon l'une quelconque des revendications 1 à 18, dans lequel les paires de bases des séquences hautement conservées sont hautement conservées par rapport à un alignement des VAA 1,2,3,4,5 et 6 et des VAA isolés à partir d'oies et de canards.

20. Procédé selon l'une quelconque des revendications 1 à 19, dans lequel la séquence variable est une séquence hypervariable.

21. Procédé selon l'une quelconque des revendications 1 à 20, dans lequel la première région comprend jusqu'à 10 kilopaires de bases en longueur.

22. Procédé selon la revendication 21, dans lequel la première région comprend un fragment de 3,1 kilopaires de bases comprenant toute la longueur de la séquence du capsid.

23. Kit pour détecter la présence d'un virus associé à l'adénovirus (VAA) inconnu dans un échantillon d'ADN cellulaire dont on suspecte qu'il contient une infection latente par un VAA, ledit kit comprenant:

- (a) une première série d'amorces qui amplifient spécifiquement une première région comprenant 250 paires de bases de séquences d'acides nucléiques d'un capsid de VAA, ladite première région présentant au moins 18 paires de bases d'une séquence hautement conservée en son extrémité 5', une séquence variable et au moins 18 paires de base d'une séquence hautement conservée en son extrémité 3', lesdites paires de bases étant hautement conservées par rapport à un alignement d'au moins VAA1, VAA2, VAA3, VAA4, VAA5 et VAA6;
- (b) éventuellement une deuxième série d'amorces spécifiques d'une deuxième région des séquences d'acides nucléiques de VAA qui comprend la première région des séquences de VAA et des séquences qui se situent côté 5' par rapport à la première région, de manière à obtenir des séquences d'extension 5' des VAA qui hybrident sur l'extrémité 5' des séquences de VAA amplifiées par les amorces pour la première région ;
- (c) éventuellement une troisième série d'amorces qui amplifient spécifiquement une troisième région, qui comprend la première région de séquences de VAA et des séquences qui se situent côté 3' par rapport à la première région, de manière à obtenir des séquences d'extension 3' de VAA qui hybrident sur l'extrémité 3' des séquences de VAA amplifiées par les amorces de la première région;

chacune desdites deuxième et troisième région étant prédéterminée sur base de l'alignement des séquences d'acides nucléiques d'au moins les VAA1, VAA2, VAA3, VAA4, VAA5 et VAA6, et chacune desdites régions comprenant des séquences d'acides nucléiques qui sont hautement conservées sur au moins 18 paires de bases en l'extrémité 5', éventuellement des séquences variables au centre et des séquences qui sont hautement conservées sur au moins 18 paires de bases en l'extrémité 3' des séquences de la région, par rapport aux séquences au moins des VAA1, VAA2, VAA3, VAA4, VAA5 et VAA6;

chacune des séries d'amorces étant constituée par une amorce 5' et une amorce 3', chacune desdites amorces comprenant au moins 15 nucléotides complémentaires à sa séquence respective hautement conservée et présentant une identité exacte avec sa séquence respective hautement conservée sur au moins 5 paires de bases en son extrémité 3'.

24. Kit selon la revendication 23, dans lequel l'amorce 5' et/ou l'amorce 3' comprend au moins 18 nucléotides.

25. Kit selon la revendication 24, dans lequel l'amorce 5' et/ou l'amorce 3' comprend 25 nucléotides.

26. Kit selon l'une quelconque des revendications 23 à 25, dans lequel l'amorce 5' et/ou l'amorce 3' comprend au moins

9 paires de bases d'identité exacte en son extrémité 3'.

27. Kit selon la revendication 26, dans lequel l'amorce 5' et/ou l'amorce 3' comprend au moins 18 paires de bases d'identité exacte en son extrémité 3'.

5

28. Kit selon l'une quelconque des revendications 23 à 27, dans lequel la première série d'amorces permet l'isolement de toute la longueur des séquences de capsid d'un virus associé à l'adénovirus d'un échantillon, la première série d'amorces comprenant une amorce 5' dirigée sur une région localisée au centre d'un gène rep d'un VAA, basée sur une région prédéterminée conservée d'un VAA et une amorce 3' dirigée sur une région en aval d'un gène cap d'un VAA, basée sur une région prédéterminée conservée d'un VAA.

10

29. Kit selon la revendication 23, dans lequel l'amorce 5' présente une séquence comprenant GCTGCGTCAACTG-GACCAATGAGAAC, ce qui correspond aux nucléotides 1398 à 1423 de la SEQ ID NO:6.

15

30. Kit selon la revendication 23, dans lequel l'amorce 3' présente une séquence comprenant CGCAGAGACCAAAGTT-CAACTGAAACGA, qui correspond aux nucléotides complémentaires à 4462-4435 de la SEQ ID NO:7.

31. Kit selon l'une quelconque des revendications 23 à 30, dans lequel l'échantillon comprend un VAA intégré dans le chromosome.

20

25

30

35

40

45

50

55